

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 94616

TO: Manjunath N Rao

Location: CM!/10A11/10D01

Art Unit: 1652

Thursday, May 29, 2003

Case Serial Number: 922683

From: Paul Schulwitz

Location: Biotech-Chem Library

CM1-6B06

Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (703)305-1954



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Rao, Manjunath N.

Sent:

Wednesday, May 21, 2003 1:54 PM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search request for 09/922683

From: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10D 01

Phone: 306-5681

Date: 5-21-03

Please search the following as soon as possible for application with serial number 09/922683

1. SEQ ID NO: 7, against all <u>commercial nucleic acid databases</u> including <u>issued patents database</u> and <u>pending</u> <u>application database</u> and provide a <u>print of all results</u>.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D. Biotechnology Patent Examiner Art Unit 1652, Room 10A11 Mail Box in 10D01 Crystal Mall 1, USPTO.

POINT OF CONTACT:
PAUL SCHULWITZ
TECHNICAL INFO. SPECIALIST
CM1 6B06 TEL. (703) 305-1954

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:	NA Sequences:	STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up: 5/13	Bibliographic:	DRLink:
Date Completed: 5/29	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
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OM nucleic - nuc Run on: Title: Perfect score: Sequence: Scoring table: Coring table: Total number of I Minimum DB seq 16 Maximum DB seq 16 Post-processing:	Copyright (c) 1993 - 2003 Compugen Ltd. nucleic search, using sw model May 28, 2003, 15:28:40; Search time 11321 Seconds (without alignments) 17619.524 Million cell updates/sec US-09-922-683-7 6854 : LTGAGGGGTTCCCTGGTGCATCGAGCCGATCCGGCTGCAG 6854 : IDENTITY_NUC Gapop 10.0, Gapext 1.0 2054640 seqs, 14551402878 residues of hits satisfying chosen parameters: 4109280 q length: 0 q length: 0 q length: 0 q length: 2000000000 ng: Minimum Match 0% Listing first 45 summaries GenEmbl:*
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	CCTCG1		CAAGGC	CAGTGC	SAACCI IIIIII SAACCI	SACCAC	28CGG7	GTGGAJ GTGGAJ		6854 bp us 6306627			sis ge ens GI OCT-2(a = 6	core 6854; red. No. 0; Mismatches	CCCTGC	GTGAGC	TCCTTCTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TGCAGG
	AAGGA	CAGAA(GACGTO	000000000000000000000000000000000000000	TCGAA(TCGAA(CAGCA(CAGCA(TCCGT) - - - -					ynthe: ucesco	ocation/waiiileis 6854 'organism="unknown" 2445 c 2445 g	υ _α				GGTCG
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	Accec	SGAACA SGAACA	366CCA	000000	GTACG	CAAGG	ACGAGG IIIIII ACGAGG	AGGCCG HHHH AGGCCG	68	from	GI:1	Unknown. Unclassified. (bases 1 to 6854)	of the comyce 63066	685 organi 2445	/at	716616	GCGAT	AGCCG	SAGCAC
	CGCCT	CGGCT(367CGC	CTCGG	CTCCG(CTCCG(CGTCTZ	CGACA CGACA	GCTGC2 - - - GCTGC2	057 nce 7	057.1	wn. ssific ases	r,H. tion (strepi t: US	18 a / 1	larit; Conse	GTTCC(GTTCC	ATGTCC ATGTCC	TTGACC	CAGAA
	GTGTGCGCGCCTACCGCGTCATCAAGGACCTCGTGGACAGCAAGGCGGCCATCACCGACG	CGTCCGACGGCTGGAACAACATGCAGAACGCCTTCAAGTCGGGCAAGGTCGCCATGATGG 	TCAACGGCCCCTGGGCCATCGAGGACGTCAAGGGGGGAGCCCGCTTCAAGGACGCCGGCTT	ACCTGGGGGTCGCCCCCGTCCCGGCCGGCAGTGCCGGACAGGGTCTCCCCCAGGCGGGTTTTTTTT	GGAACCTCTCGGTGTACGCGGGCTCGAAGAACCTCGACGCCTCCTACGCCTTCGTGAAGT 	ACATGAGCTCCGCCAAGGTGCAGCAGCAGCACCACCGCGAGAAGCTGAGCCTGCTGCCACCC	GCACGTCCGTCTACGAGGTCCCGTCGCGGACAACGAGATGGTGAAGTTCTTCAAGC	CGGCCGTCGACAAGGCCGTCGAACGGCCGTGGATCGCCGAGGGCAATGCCCTCTTCGAGC 	CGATCCGCTGCAG 	AR174	AR174057 AR174057.	Unknown Unknown Unclass	Decker, H. Isolation of the biosynthesis genes for p from streptomyces glaucescens GLA.O, and Patent: US 6306627.A 7 23-CCT-2001;	101	sh Simi	CTGCAGGGTTCCCTGGTGCACCCGCCCTGGTCGACGACGAGGCGCTGTCGCAGAT	CGCGGCGATGTCGCGGGGTGGTGGTGGTGGCCCCCCCCCC	GGCGCGGTTGACCGCCGCGCACCGCGTCTTCAGCACCATGTCGAGGCCGATCGTGGGG	CTCGTCCCAGAACAGCACGGCCGGGTCGTGCAGGCTCGCCGCGCGCG
	6361 GT	6421 CG 6421 CG	6481 TC 		6601 GG 	6661 AC 6661 AC	6721 GC 6721 GC	6781 CG 	6841 CG 			_		an.	Query Match Best Local Similarity Matches 6854; Conser	1 1			
) qq	79 qa	Oy 64	Oy 65	Oy 6(Qy 6(Oy 67	Oy 67	Qy 66 Db 66	RESULT 2 AR174057 LOCUS DEFINITIC	ACCESSION VERSION KEYWORDS	ORGANISM	AUTHORS TITLE JOURNAL	BASE COUNT	Quer Best Matcl	Qy Dp	් දුරු සි		
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                                                                                                               PGCAGCGGCCGGAGGTGGGGGTCATGATGCCGGTCAGCATCTTGATCGTGGTCGACTT
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1261	1321	1381	1441.0	1501 (1561 (1621 (1621 (1681	1741 (1801	1861 2	1921	1981 1981	2041 0	2101 7	2161 C	2221 C	2281 T	2341 T 2341 T
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Qy Dp	2401	GTCGTGGGGGGCGTA
δλ dd	2461	GTTCGGGTTACGCATACCTCCACCGCCCCGCCCGCTCGGTC 25:
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, oy	2761	TICGCGCTCATCGGCGTGTACGCCTTCAGCCCGGCCGTCCACGAGGCGGTACGGGCCA 28
ò	82	CACCCCTCCGCCGCGGGGAGCTGGAGATCACCCCCCCCCC
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ογ O	2941	AGGACATGCTGGAGGTCAACGTCACGTCCTGGACGGACTGGAGGGCGCATCGAGGGGA 3000
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Q		36661CACACGTGGTGGGCCCGGTGATCGGCGCGGGTGCCGTCGTCAGCAACTCCA 312
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οy	18	rca 324
đ	3181	CCGTCCTGCTGCGCGCGCCCCAGGTCGAGGGGGGCGTCCCGCATCGAGGCGTCCCTCA 3
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GTCCA	ATCGT	SCGCAC	SGCGGA 11111 SGCGGA	CTCAT	SAACAA SAACAA	CTGTC	GTCGA IIIII	CTACAA CTACAA	ACTGTG 	SCGCTA SCGCTA	CTTCGC	rcccri 	ACCGCC 	099090	099090	SCCTTG	rcgrcc
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CCCGATTCCGGGATCACTCAGGGGAGTTCACAATGCGGCGTGGCATTGCGGCCACCG GCGCCCGGTCGTCGTCGGGGAAGGTGCCTCGATCCGGGGCGAGAACCGTTC TCGGGGGTGACCAGTCCGACCAGCTCGGCGCGCGCGTGTCGCGCCGGCTGCTCGTAG AGCGCGTCCAGTGCGGTCACCGAGTCGCGGGTGCCGGTGGCCACACCGCGCGCA TTCAGCACCCGGCTGACCGTGGCCTTGCTGACGCCCGGGCCTGCGATGTCGGCG AGGACGAAGGCCACCTGCCGCTCGTGCAGCCGGCCGTACCGTCCGGTCTCGGCGGTG TGACGCGTGAGCGCCTGCCCCATCACCTGGGCCAGTGCGGGGAAGAAGGGGGTTGTCC TGGCTGAAAATGCTTGCAGCAAATTGCCGCAACGTCTTTCGGCGGCGTTTTCGATCCT **ACCITICCTGGCAACCCCGGCGCGCGCAGAAGCGGTTGGCCGTGAGGCGTCCAGACCT ACGECGAGECCGACGCGCTCGTGCCCCAGCTCCGCCAGGTGCGCCACGGCCAGGCGC** GCGCCCCGGTCGTCCGGGGAGACGAAGGGTGCCTCGATCCGGGGCGAGAACCCGTTC

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9	5701 5701	5761 5761	5821	5881	5941	6001	6061	6121	6181 6181	6241	6301	6361 6361	6421	6481	6541	6601	6661	6721 6721
qa	Oy Op	දු පු	Oy Op	Q Q	Ş	ç d	Qy Op	oy Op	Oy Op	Oy Dp	Qy Dp	oy da	6 G	9. 9.	S S	Qy Dp	Oy Dp	Qy

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AF237894S1 9523 bp DNA linear BCT 26-MAR-2000 Streptomyces antibioticus Tu99 oleandomycin biosynthetic gene cluster, partial sequence.
AF237894 GI:7329189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinobacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomyclneae; Streptomycetacese; Streptomyces.
1 (bases I to 9523)
Draeger,G., Park,S.-H.H. and Floss,H.G.
Mechanism of the 2-deoxygenation step in the biosynthesis of the deoxybraxose moleties of the antibiotics granaticin and oleandomycin.
2 (bases I to 9523)
Park,S.-H.H., Sohng,J.-K.K., August,P.R., Niggemann,J. and
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arfaaafgcbavpgrgalldrddinnlyvelpvwytpewybballrgrhyverplta
resgaedlialarsrguymmertslhhaohgtvydlindgtigelrslsaaftipp
pegdiryopdyggalldigtyplraalhflepdlaagavlrrerrrwyvysghvil
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GRRYLLADVLOSEQGSWFLHKRNRNBWEALDDVPLDDDFHW1SLGGLRKLLIFRHLV
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HVPFRELSGWQFDENTGNLRHTSGRFFSIEGLRVRTDHCWFGSWTQPIIVQPEIGILG
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Bark, S.-H.H., Sohng, J.-K.K., August, P.R. and Floss, H.G.

Direct Submissel 2000) Chemistry, University of Washington, Box
351700, Seattle, WA 98195-1700, USA
1. 1054203
/db_xref="taxon:1890"
complement(167...153)
/note="Orfl1; involved in the 2-deoxygenation step in
dTDP-L-oleandrose biosynthesis"
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/note="Orf10; involved in the 2-deoxygenation step
dTDP-L-oleandrose blosynthesis"
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/transl_table=1.1
/roduct="dTDP-3,4-d1keto-2,6-d1deoxyglucose
3-ketoreductase"
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/db_xref="G1:7329191"
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ALTRQTLDRQPGLWDLYALRTSLYGLSEDDYVATTTKKGAFQRVKDNLTRFQALRRER
EAPVRLGLNYI ILFGRAGRLTGLADYFADLMDAAPDREVDFLTLREDYSGRPGKLAP
ERVELEHGLAAFEERI RRTRAPSLHVOYGYALQSLRGVDAELPRIRPETAHPQ
VANQYDLLGDYYLYREAGFPGLQGARRYVAGRLTTGTELEEVVRRFVTEGRQVAPRPG
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                                                                                                                                                                                              /translation="MALQVDRTPLDPIAVCAWPGGNSAAAALRPLIEEDAPGTGLEP
DATABELIALARRYGTEPFTPLESARRGAGLOFATFARTLAVEWFRRTPALRATAVERRPA
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llarity 67.9%; Pred. No. 1.2e-66;
Conservative 0; Mismatches 658;
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/db_xref="G1:7329198"
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/transl_table=11
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MONGSVSRKGVLRGIHFADAPPQGARYTVGAGGTVLDVVDVRRGSPFGRWAAVRLD
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IVLSAKDTHAPSLAQAAETGILDDYEBCRAYTARAAGYGPAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKALVLAGGSGTRLRPITHTSAKOLVAVANKPVLFYGLEAIAAA
GIDTVGLIVGOTAGESFRAAVOOGAKFGLLDIYTIGOSPELGLIAAVLLAHTYLGDDDFV
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RHPKSDLALVGVYFFTPAIHEAVRAIEPSWRGELEITHAIOHLIDDGRVGNYTEGY
WKDTGWNADALEVWRFVLEDLEPRIEGTVDEHIVVIGRVVVGEGARTINSRIMGPAI
GAGREISDSYIGPFSSVGDNCHITGSEMEFSIMLAESAITGVRRIEGSLIGRNVQVTO
SLHAPNAHRPVLGGHSKVEIQS"
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Vignypddpaytfyrgdiadaplydslimaeadqyvhfaaeshydrsifspgtfyrtny
Leydyllidbaclrhgyrgyryrygjergsiergswergplichspysaskassdlla
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DDHCLGYDLYRTQGRPGEYYHIGGGTELTNRDLYGLLDAFGYGWDYYDPYADRKGHD
RRYALDCAKAADELGYRPRRDFAEGIARTIDWYRDNRAWWEPLKKRPAGPAAPRGAAA
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AAAERHRGTYVNCAAYTAVDDAETDEAAAALLNAEARALFAEACAPHGARLVHLSTD
YVFFGDARPFYARPTARBASVGREKREDGEAALTALPTATVLRTAMLYGRTGREY
RTMIEREARGGAIDVVADQCGQPTWTGDLADKIIAVGRHPGYHGILAATNAGSATWYD
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RWLTNGGPLVREFEORIADLAGVRNCVATCNATAGLQLLLREAEVTGEVIMPSWTFVA
TAHAVRWLGLRPVFCDIDPDTGCLDPKLVEAAVTPRTGAILGVHLWGRPSPVDELAAI
PVGPGLAAFVTRRIRGVLHVLLHARTEAGLLNGPEMAPTVQCRPLNYRAVPAEYRPAY
LDYVLSADPGRIRYDTLQSEEGGRFHHAENRYVVVEAEDDFPVEVPRDFRWLTLHQIL
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                                                                          Involved in the 3,5-epimerization step. dTDP-L-oleandrose biosynthesis"
                                                                                                                                                                       /product="dTDP-4-keto-6-deoxyglucose 3,5-epimerase"
/protein_id="AAF59933.1"
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/transl_table=11
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/protein_id="AARF5995.1"
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/protein_id="AAF59937.1"
/db_xref="GI:7329197"
                                                                                                                                                                                                                                                                                                                                                                                                                /product="dTDP-D-glucose synthase"
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                                        ALLHHSNYVNVEARSLVACIQALS"
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/note="Orf9; involved in
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GGTVISGSYIGPFTSVSEGCRIEDSEIEFSIVLRDSRVRGVQRVRGSLIGRSVVVAPA
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CGGGCCCGGAGCGCATCGTCCACGTCGAGAACCGCAAGGGGGCACGACGGCGCTACGCGG
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Inclinal, Julian Claveria S/N, 33006 Oviedo,
3 (bases 1 to 2404)
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                                                                                                                                                                                                                            Length 2404;
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Pred. No. 8.6e-66;
); Mismatches 647;
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PRKPAGTRLVLGDHSEGQISS*
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/gene="mtmE"
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                                                        /codon_start=1
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/gene="mtmE"
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ilarity 68.0%;
Conservative
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/translation-"MTTSILVTGGAGFIGSHYNRTLLGPRGYPDVTVTUDKLTYAG
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LHYDDHVRAIELVRTGGRAGEVYNIGGGTELSNKELTQLLLDACGAGWDRVRYVTDRK
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IVEQVDTEAVLRSAANARLGVDVEWETRLTGFSQDAEGUDYTLEHADGTTESTRVPWLV
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HENSDMAVICOYYLFYPLVHENTALIEPSMGCELEITHALQUALDNRHNYSTVTHGYW
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SGTVISGSYIGPYTSVSEGCRIEDSEIEFSIVLRDSRVRGVORVRGSLIGRSVTVAPA
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GTRFEEVASGDWRGFLDDNLAPTLRTVQLVVAGWRARSWGRIVLISSHVALDGHRGQE
FYGAAKSALHGFARSLAWDVGRDGVLVNVVCPGLTTTERVLTGLPDEIRERELGSTPT
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                    Salas, J.A.
Direct Submission
Submitted (03-UUL-2000) Salas J.A., Biologia Funcional Universidad Submitted (03-UUL-2000)
Submitted (03-UUL-2000)
Submitted (03-UUL-2000)
Salas J.A., Biologia Funcional Universidad de Oviedo, Julian Claveria S/N, Asturias, SPAIN
On Jul 5, 2000 this sequence version replaced g1:3334818.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="dTDP-glucose synthase"
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/gene-"mtmTII"
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/gene="mtmE"
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(bases 1 to 18977)
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/gene="mtmE'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCT 26-FEB-2002
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Submitted (14-JUL-1998) Salas J.A., Biologia Funcional Universidad
de Oviedo, Julian Claveria S/N, Asturias, SPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ007932.2 GI:8926774
AJ007932.2 GI:8926774
acyl carrier protein; acyl CoA ligase; aromatase; cyclase;
b-mycarose 2,3-dehydratase; D-mycarose 3-C-methyltransferase;
D-oilose 2,3-dehydratase; D-oilose 4 ketoreductase; D-oilvose
2,3-dehydratase; dTDP-glucose 4,6-dehydratase; dTDP-glucose
3,3-dehydratase; mtDP-glucose 4,6-dehydratase; dTDP-glucose
mysthase; ketoacyl synthase; ketoacyl synthase; ketoacyl synthase; ketoacyl synthase; mtLD gene; mtLT gene; mtLTI gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lombo, F., Blanco, G., Fernandez, E., Mendez, C. and Salas, J.A. Characterization of Streptomyces argillaceus genes encoding a polyketide synthase involved in the biosynthesis of the antitumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning and insertional inactivation of Streptomyces argillaceus genes involved in the earliest steps of biosynthesis of the sugar moieties of the antitumor polyketide mithramycin J. Bacteriol. 179 (10), 3354-3357 (1997)
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                                                       4185
                                                                                                                                                                                                   2047 CACGAAGATCCGGCGTGAGCTCGGGTACCGGCTCGGGAGTTCGGGGACGCACTGGC 2106
  1927 CACCGAGCTGTCCAACAAGGAGCTGACGCAGCTGCTCCTGGACGCCTGTGGCGCCGGCTG 1986
                                                                                 Lombo,F., Slems,K., Brana,A.F., Mendez,C., Bindseil,K. and
Salas,J.A.
                                                       4126 GGAGCGCATCGTCCACGTCGAGAACCGCAAGGGGCACGACCGCCGTACGCGGTCGACCA
                                                                                                                                                                      4186 CAGCAAGATCACCGCGGAACTCGGTTACCGGCCGCGCACCGACTTCGCGACCGCGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes.
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Streptomyces argillaceus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                      2107 cGAGACTGTCGCCTGGTACCGCCACCACCGTGCTGGTGGGAGCCGCTG 2155
                                                                                                                                                                                                                                                                                  4246 CGACACCGCGAAGTGGTACGAGCGGCACGAGGACTGGTGGCGTCCCCTG 4294
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complement(4970. .5269)
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Length 18977;

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Query Match

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                       CCTCGTCACCGGCGGAGCGGGCTTCATTCGCTCCGCCTACGTCCGCCGGCTCCTGTCGCC
                                                                    3406 CGGGGCCCCCGGCGGCGTCGCGGTGACCGTCCTCGACAAACTCACCTACGCCGGCAGCCT
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BCT 06-JUL-2000

AF055579 Innear BCT 06-JUL-20 Streptomyces antibioticus putative 3-Ketoreductase (olew), 2,3-dehydratase (oleV), dTDP-4-keto-6-deoxyglucose 3,5-epimerase (oleL), dTDP-b-glucose synthase (oleS), dehydratase (oleE),

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AREAARGCERVPGALLDRDDIDALYVPLEVWHTPWVEAALLGGHVVLOURGEPUTA
TRSGAEDLIALARSRGLVLMENFTSLHHAQHGTVTDLLRDGTIGELRSLSAAFTIPPK
PREDIRYQPDVGGGALLDIGIYPLLALHFLEGPDLHAAGAVLRERRRNVVVSGHVLL
PTPHGVVAELARGEHRAYSEYTLFGTAGRLALDRARFPEFHRPRVEIHRQDALDIV
DLPPDAQFANLVKDEVLAVREGPGRLTCHHADAVRQADLVERVWAVARVRWC"
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Identification and expression of genes involved in blosynthesis of L-oleandrose and its intermediate L-olivose in the oleandomycin producer Streptomyces antibloticus
Antimicrob. Agents Chemother. 44 (5), 1266-1275 (2000)
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Quiros, L.M., Aguirrezabalaga, I., Olano, C., Mendez, C. and Salas, J.A.
Direct Submission
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1 (bases 9806 to 15052)

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2 (bases 9806 to 15052)

3 (bases 9806 to 15052)

4 (bases 9806 to 15052)

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Quiros, D.M., Aguirrezabalaga, I., Olano, C., Mendez, C. and Salas Direct Submission 1999) Departamento de Biologia Funcional e Instituto Universitario de Oncologia de Asturias (I.U.O.P.A.), Onlaversidad de Oviedo, Oviedo 33006, Spain Sequence update by submitter on Sequence update by submitter on Sep 16, 1999 this sequence version replaced gi:3023163.
4-ketoreductase (oleU), dehydratase (oleNI), reductase (oleT), glycosyltransferase OleI (oleI), aminotransferase (oleN2), and glycosidase OleR (oleR) genes, complete cds.
AF055579
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Streptomyces antibloticus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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/protein_id="AAD55450.1"
/db_xref="G1:5902166"
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/product="2,3-dehydratase"
/protein_id="AAD55451.1"
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/gene="oleV"
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/db_xref="G1:5902168"
//db_xref="G1:5902168"
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AARHQGLYLAGGIGHAFMALTDDAATVYYLCSQPYVARBERAVDPLDPAIGIEWPTDID
IVPVGEGTPTHRPWRRPRRFGILPDYEGVPGALHRGGGRRGTGP"
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//Lranslation="%KALVLAGGSGTRLRPITHTSAKQLVAVANKPVLFYGLEAIAAA
//Lranslation="%KALVLAGGSGTRLRPITHTSAKQLVAVANKPVLFYGLEAIAAA
//Lranslation="%KALVLAGGSGTRLRPITHTSAKQLVAVANKPVLFYGGLDDDFV
MYLGDNFIVGGTDDDFVRTFRCGRRPAARILITHVSDPSGFGVAELDDDGRVVGLEEKP
RHPKSDLALVGVYFFTPAIHEAVRAIEPSWRGELEITHAIQHLIDNGADIQSWVIEGY
WARDTGWNADALEVNRRVLEDLEPRIEGTVDEHTVVIGRVVVGEGARYTNSRIMGPAII
GAGPBISDSYIGPPFSVGDNCHITGSEMEFSIMLAESAITGVRRIEGSLIGRNVQTQ
SLHAPNAHRFVLGDHSKVEIQS
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VLGTVPLDDAALRHOVGPFVHYSTDBYYGSIEHGSWPEHQPLCPNSPYSASKASSDLLA
LSTYPLTGLDVRYTRCSNVYBPNYSTDBYYGSIEHGSWPEHQPLCPNSPYSASKASSDLLA
LSTYFTHGLDVRYTRCSNVYBPNYBPREKTVPLLAFTNALLOGLRYPLYBOGLNYREWLHY
DDBCLGVYDLVYRTGGEREYTHIGGGTELTNRDLTGLLLDAFGVGWDVVDPVADPRAKGHD
RRYALLOCAKAADELGYRPRRDFAEGIARTIDWYRDNAWWEPLKKRPAGPAAPPRGSG
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/translation="MRWLITGAAGMLGRELVRRLAENEEDVAALGHDHLDVTRPSAVR
AALAEHRPGIVVNCAAYTAVDDAETDEAAAALLNAEAPRLLAEGLRPHRRHGLVHLST
                                                                                                                                  SRRELVQORVPLEETAFSGWRRDDHAIAHKDGDYFRYIGVSYRASSREVSSWSOPLIA
PVGPGLAAFVTRRIRGVLHVLLHARTEAGLLNGPEMAPTVQCRPLNYRAVPAEYRPAY
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HVPFRELSGWQFDENTGNLRHTSGRFFSIEGLAVRTDHCWFGSWTQPITYQPEIGILG
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GRGRVLADVLQSEQGSWFLHKRNRNMVVEALDDVPLDDDFHWISLGGLRKLLLRPHLV
                                                                                                             NMDTRTVLSCLPPDPAPDGROPPAPAAPFAAAVTRSLTRGATALHTMGEILGWLTDER
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                                                                                                                                                                                                                                                                                                                                                  5 in the
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/protein_id="AAD55453.1"
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biosynthesis of L-oleandrose"
/codon_start=1
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                                                                                                                                                                                                                 ALLHHSNYVNVEARSLVACIQALS"
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/db_xref="G1:5902170"
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/transl_table=11
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/gene="oleL"
3356. .3970
/gene="oleL"
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/gene="oles"
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/gene="oles"
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5034. .6041
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/gene="oleU"
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LTDGNAMFASLIDRMPTDNPHALYLSGGLEPLTNPGTGDLVRRAARGEKLSLYTNSE
ALTRQTLDRQPGLWDLYALRTSLYGLSEDDYVATTRKGAFQRVKDNLTRFQALRRER
RRPVRLGLINY I ILPGRAGRLYGLADY GDLNDGGPDRPVDFLYLREDY SGRPGGKLAP
BENYLLEHGLAAFEERI RRTRAPSLLYDYGYALQSLRGVDAELPRI RPETWRPTAHPQ
VANQYDLLGDYYLY FRAGFPGLQGABRYVAGRLTTGFELEEVVRRFVTEGRQVAPRPG
EEYFLDGFDQTVTARLNQMETDI ADGWAEHRGFLR
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;
DYVEPGDART PYAEDHPTAPRSAYGRTKRDGEQAVLTALPTATVLRTAMLYGRTGRSF
VRTMI EREARGGAIDVVADQRGQPTWTGDLADRI I AVGRHPGVHGI LHATNAGSATWY
DLAQEVFRLLIDADPGRVRPTTGAAFRRPAPRPAY SVLGHDRWRGTGLAPLRDWRSALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERLRALHNFCLGHDGVGAGINAKMSEAAAAMGLTSLEAFADAVASNRANYELYRQELS
GLPGVRLIDYDPAERNNYHYVIALIDAGVTGLHRDLLLTLLRAENVVAQPYFSPGCHQ
REPYRTEHPVSLPHTEHLAEQVIALPTGPAVSREDIRRVCDIIRVAAAHGPRITAQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="possibly responsible for the 3,4-reduction step
in D-desosamine biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKRGVHDLALFGGDAAFLQPLYMGRPNTGDRKRLLDRLEWALDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWLTNGGPLVREFEQRIADLAGVRNCVATCNATAGLQLLLREAEVTGEVIMPSMTFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAHAVRWLGLRPVFCDIDPDTGCLDPKLVEAAVTPRTGAILGVHLWGRPSRVDELAAI
AAEHGLKLFYDAAHALGCTSRQRRLGSFGDAEVFSFHATKVVNSFEGGGIVTDDDTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MALQVDRTPLDPIAVCAWPGGNSAAAAALRPLIEEDAPGTGLEP
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GMYWTNT I LPLERRGVLDAAVRGEPAFPY SVGLYPGPSCMFRCHFCVRVTGARYQOSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9957. .11231
//gene="ole:"
/function="intracellular inactivation of oleandomycin by
glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2447
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                                                                                                                                                                                                                  /function="possibly involved in the transamination, together with oleN2, during the biosynthesis of D-desosamine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCGCCAAGCAGCTGCTCCCCATCGCCAACAAGCCCGTGCTCTTCTACGCGCTGGAGTCC
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67.7%; Pred. No. 9.4e-66;
:ive 0; Mismatches 656;
                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
/product="dehydratase"
/protein_id="AAD55456.1"
/db_xref="GI:5902172"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="reductase"
/protein_id="AAD55457.1"
/db_xref="GI:5902173"
                                                                                  EAFPDILAAEHPPTRRGAA"
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/transl_table=11
                                                                                        /gene="olen!"
/gene="olen!"
6922.
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/gene="oleNI"
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8225. .9682
/gene="oleT"
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/gene="ole!"
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                                                                                    GTCGTCAGCAACTCCAGTGTCGGCCCGTACACCTCCATCGGGGAGGACTGCCGGGTCGAG
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TICCTGCTGTACCTGGGGGACAACTACCTGCCCCAGGGGGTACCGACTTCGCCCGCAAA
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                                                                                                                                         GAGGCGGTACGGCCCATCACCCCCTCCGCCGCGCGAGCTGGAGATCACCCACGCCGTG
                                                                                                                                                 CAGTGGATGATCGACCGGGGCCTGCGCGTACGGGCCGAGACCACCACCCGGCCCTGGCGC
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                                                                                                                                                                                                                                                                                                                             GACAGCGCCATCGAGTACTCCGTCCTGCTGCGCGCGCCCCAGGTCGAGGGGGGGCGTCCCGC
                              TTCGTCATGTACCTGGGCGACAACTTCATCGTCGGCGGCATCGACGACCTGGTCCGCACC
                                             T---CGGCCGCCGATCCCGCGGCGGCCCGGCTGCTCACCCCGGTCGCGGACCCGTCC
                                                                           GCCTTCGGCGTCGCGGAGGTCGACGCGGAACGTGCTGCGCTTGGAGGAGAACCC
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strK gene; strL gene; strM gene;
strQ gene; strR gene; strS gene;
strW gene; strX gene.
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                                                                                                                                                                                                                                                                                                     ACCAGCATCCCGAGAAGCTCATACCGCGCTTCCTGACCAGCCTCCTGTCCGGCGCCACCG
                                                                                                                                                                                                                                                                                                                                                                                            TTCCCCTCTACGGCGACGGCGCACGTGCGCGACTGGCTGCACGTCGACGACCACGTCA
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Streptomyces glaucescens GLA.0 gene cluster for 5.7-hydroxystreptomycin blosynthesis.

AJ006985.1 GI:3256042

Sph gene; strA gene; strB1 gene; strB2 gene; strD gene; strP gene; strQ gene; strY gene; 
TGGGCACCCAGGTCCTGCTCGACGCCGCGCTCCGCCACGGTGTGCGCACCTTCGTGCACG
                                                                                    TCTCCACCGACGAGGTGTACGGCTCCCTCCGGCACGGGGCCGCCGCGGAGAGCGACCCCC
                                                                                                                                                                                TGCTTCCGACCTCGCCGTACGCGGCGTCGAAGGCGGCCTCGGACCTCATGGCGCTCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGCCGTCGAACTCGTCCGCGTGTCGGGCCGGCCGGGAGAGATCTACAACATCGGGGGCG
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SGAJ6985
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DEFINITION
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PGVQGNLLRFVRGLGVTPLVAGNVKGLQDEYRTPATQKAFAERWGQNVHMYTSFADGT
KVSFEGAIYANAHGLIYVARRGMYGRGHTGHYDELTGYYDIDELRELGGVUDVVVGARP
GPGYVYIGTHDDPRQRHYLELYKLGKGPLYSFYTHCHFEVPHTIARAVDFADAAL
TPPAGPRUDVVATARRDLKAGTVVDGIGGYDTYGVAETHAATLASRLLPMGVAEGCVL
RRDIARDAVLTYDDVRLPAGRLVDRLREEQNELFFG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:054202"
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/translation="MLIHETPLAGAALIELSELRDERGFFSRSFCREEFERAGLEPAV
VQCNLSFNHRAGSLRGFHYQTEPNAEAKTIRCTRGAIYDVIVDLRPDSPTFLRHFGAE
LTADNRLALHVPRNTAHAYLTLADDTETVYQVSAAYTPGAERGLRWNDPALGVEWPAP
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APLQRLARDRQLTLHPHHDFWCAMDTFKDYQHLNELWAAGDAPWKVWEQPGNRSVSPG
TARSAPRAAGRPAAVRRHR"
                                                                                                                 /note="The expression of both the genes, strX and strV, is activated by binding of the protein StrR" /citation=[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mtvDSDIPVVLLCGGYGTRIREASERLPKAMVDIGGRPILWHIM
KIYSHYGFRRFVLCLGYKGWAIKQFFLDYRAQLSDFTISLSDEHRIRFHDDRADENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MITVDTALRRREERDRPIRVGMYGAGFMGRGLARHIVRSVPGMR
LAAIANRSLATAERAYTEAGVRPVRANGAGDVEAAVAAGRPVYTEDAFALLAAEGIDC
LVDVTGAVEFGARVTVAALERGLPVVTMNAELDGTVGPLLAHRARAAGVVLTAADGDQ
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                                                                                                                                                                                                                                                                                                                                                                                     'function="putative 5'-hydroxystreptomycin biosynthesis
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                                                                                                                                                                                                                          /function="StrR binding site"
/evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:054201"
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                                                                                                                                                                                              bound_moiety="activator"
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'protein_id="CAA07375.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Strx"
/protein_id="CAA07373.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA07374.1"
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                                                               3587. .3615
/gene="strV and strX"
                                      and strx"
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/gene="strv a
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'gene="strX"
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'qene="strU"
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/gene="strx"
3706. .4254
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  Beyer, S., Distler, J. and Piepersberg, W.

The str gene cluster for the biosynthesis of 5'-hydroxystreptomycin in Streptomyces glaucescens GLA.O (ETH 22794): new operons and evidence for pathway specific regulation by StrR Mol. Genet. 250 (6), 775-784 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKAVGAAENAAALPDGPETVVGSGGHQLTAAQAQQIALARLVLADPHTVVLDEATALV
DPATARHTERALAAVLSDRTVIAIAHRLHTAQSADRIAVLENGRIKELGSHQELLAAN
APTPPCGAYGTAIELIAEIPRPVLA"
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AALDGSVSPGELVAFYAYAAFLVEPLGI FTETADRFARAHVAARRVVTVLRMRPKARP
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AARSGRTTVLVSSSPLLLNQADRVSFLSGGRVAAAGTHRELLAASEDYRLVIQRETGE
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/translation="MSRTRLPVAGTAEVRAHGAALARRHARDLTWMLALHGLAAVCGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGPWLIGRLLDEVVRGTTLSTVDHIGIALLLSLVAQAVLTYWAVQRSCRFGEKVTAEV
REDEVDRVVRLPLPTVEDAEPGDLITRASRDTDALTNTVRYGVPETLIALMTCLFTFA
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VEALRLQAWRRRALDRDLAEAYEAERHTWCWRSSWYLTVELSYVVPVVATLAIGGLLY
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EPVSGTVELGGVRLYDLGTEELRRRIALVTQDHHIFRGHLRENVTLARPAADDEVEHA
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/translation="MRPLPAADPGNPDIRSAARFLLWLAGRIAWPLSAAAFCGVLWLG
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                                                                                                                                                                                                                                        Piepersberg,W.

Direct Submission
Submitted (12-JUN-1998) Piepersberg W., Institut fuer Chemische Submitted (12-JUN-1998) Bergische Universitaet Wuppertal, Mikrobiologie, FB 9, Bergische Universitaet Wuppertal, Gauss-Strasse 20, 42097 Wuppertal, 42097, GERMANY
Location/Qualifiers
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/gene="strV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="putative transport of '-hydroxydihydrostreptomycin phosphate"
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5'-hydroxydihydrostreptomycin phosphate"
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Streptomyces glaucescens"/strain="ATCC 13032 (GLA.0)"
/strain="ETH 22794 (GLA.0)"
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/gene="strV"
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/gene="strW"
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/transl_table=11
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5'-hydroxystreptomycin"
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Pred. No. 1.5e-60;
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OY 3815 GCGCTCGCCACCACCGCACGCCTGGACGTCCGGGTGACCGCTGTTCGAACAAC 3874	QY 3875 TTGGCCCCCACCACCACCAGGAGAGCTCATACGGCTTCCTGACCAGCCTCCTGTCC 3934	Qy . 3935 GGCGGCACCGTTCCCTCTACGGCGACGGCGCACGTGCGCGACTGGCTGCACGTCGAC 3994 11	QY 3995 GACCACGTCAGGGCCGTCGACCGTCCGCGTCGGGCCGGGCCGGGAGACTCTACAAC 4054	QY 4055 ATCGGGGGCGCACTCGCTGCCCAACCTGGAGCTCACGCACCGGTTGCTCGCACTGTGC 4114	QY 4115 GGGGGGGCCCGGAGCGCATCGTCCACGTCGAGAACGCGAAGGGGCACGACGGGCGTAC 4174	QY 4175 GOGGTCGACAGCAGCAGCAGCGGGAACTCGGTTACCGGCCGCGCCGACTTCGCG 4234	QY 4235 ACCGCGCTGGCCGACACCGCGAAGTGGTACGAGCGGCACGAGGAGGTGGTGGCGTCCCCTG 4294	OY 4295 CTCGCCGGACATGACGTCGGACCGCAACCACCGGCCCGGCCGG	OY 4355 CCCGCGGCCGGTCGCCGGTCAGCGTCAGCGGCGGCGCCGCCCCCCGCGGGG 4114 Db 20929 GGCCGCGGCACCTGCCGGCGCGCACAGCGCCGTCCGCGGGGCACGCGC 20982	OY 4415 CGGCGGCGGTGGACCCCGG 4434 DD 20983 CGGCGCGCGCGGGGCACCC 21002	RESULT 8 AX195929/c LOCUS AX195929 109519 bp DNA linear PAT 28-AUG-2001 DEFINITION Sequence 1 from Patent WO0151639. VERSION AX195929 1 G1:15386161	Micromonospora carbonacea. Micromonospora carbonacea Bacteria; Firmicutes; Actinobacteria; Actinobacteridae	REFERENCE 1 (bases 1 to 109519) AUTHORS HOSTEd.T., HOTENTA A.C. and Wang, T.X.	AL.	Source /organism="Micromonospora carbonacea" /db_xref="taxon:47853" /db_xref="taxon:47853" ORIGIN	Query Match Query Match Query Match Best Local Similarity 56.5%; Pred. No. 7.4e-59; Matches 1892; Conservative 0; Mismatches 1402; Indels 53; Gaps 12;

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GACCGACCCGCTCCCGCGGGGGCCGAGGTGAAGGCCCTGGTCCTGGCAGGTGGAACCGGC
                                628 GAGCGCCGCCCTAGGCTCCGGCGGCATGAAGGCTCTCGTCCTGTCCGGGGGGTCGGG
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Streptomyces peucetius.
SM Streptomyces peucetius.
SM Streptomyces peucetius.
Bacteria: Firmlcutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces can to 2682)
E 1 (bases 1 to 2682)
S Gallo, M.A., Ward, J. and Hutchinson, C.R.
The dnrM gene in Streptomyces peucetius contains a naturally occurring frameshift mutation that is suppressed by another locus outside of the daunorubicin-production gene cluster
L Microbiology 142 (Pt 2), 269-275 (1996)
B 9932700
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SITEVGIVVGETSNEIRKAVGSGDRFCLRVTYLPQEAPLGLAHAVLIARDYLGEEDFV
MYLGDNFVVGGIAGNSSTFRAERPDAQILLTRVSDPSSFGVAEIGCDGRVVALEEKPR
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KDTGNVADMLEVNRAVLDGIEPGMEGQADAASELVGRVRIEAGAGIRASRIVARRHRA
GRVTDRTSALHVDRGDCSIETARSSLHHAGRLPAHGTRRVQHSLLGRNVTVAPAPRVP
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                                                                                                                                                                                                                      glucose-1-phosphate
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                                                                                                                                STMDNRLM 2682 bp DNA linear BCT 28-MAR-19 Streptomyces peucetius glucose-1-phosphate thymidylyltransferase (dnrL) gene, complete cds and truncated dnrM gene, complete cds.
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/protein_id="AAB50923.1"
/db_xref="GI:975621"
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/organism="Streptomyces peucetius"
/db_xref="taxon:1950"
/tlssue_lib="ATCC_29050"
655. 1710
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Pred. No. 4.4e-58;
0; Mismatches 676;
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/gene="dnrL"
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FRSQIAAEADFDAERSGLSPQEIRRNDRAAQFGVVTGREALADSGLDQAGLDPYRTGV
TIGSAVGAYMGLDEERRVVSDGGRLDLVDHHQYTPQHLYNHFVPSSFSFAVWANGAE
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TGLRPDGREMGEAIRVALDEARINPEAIDYINAHGSGTKQNDRHETAAFKLSLGEHAY
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ELVGEHAKSSSTELLHHGRCVLLDLADNARLREAPRLVGGVDVVTAEPHGVSEDSVLH
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FtartmevfdorgllarfgdvetsaaghfggipldfgllegawkaaktvpQsvtetsl
Eemaaelgadirrghellslrehgdavevevrgpeglrtlraaxlvgcdggrstvrka
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PRRRATPPAYEEIAAVWKRLIGGDITHGEPVWLSAFGDAARQASEYRRGRVLLAGDSA
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rglyfhtlodfdennggelieeaktddprfvaisqdlkpfiqaydpetwrspadamatrf
                                                         Streptomyces cyanogenus.

Streptomyces cyanogenus
Bacteria: Firmicutes; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycescaniomycetales; Streptomycineae; Streptomyces:
I (bases 1 to 34644)
Westrich,L., Domann,S., Faust,B., Bedford,D., Hopwood,D.A. and Bechthold,A.
                                                                                                                                                                                                                                                                                                                                                                             Universitaet
                                                                                                                                                                                               Cloning and characterization of a gene cluster from Streptomy cyanogenus S136 probably involved in landomycin biosynthesis FEMS Microbiol. Lett. 170 (2), 381-387 (1999) 99132695
                                                                                                                                                                                                                                                                                                           Vestrich, L., Domann, S. and Bechthold, A.
Westrich, L., Domann, S. and Bechthold, A.
Direct Submission
Submitted (24-JUL-1998) Pharmazeutische Biologie, Universit
Tuebingen, Auf der Morgenstelle 8, Tuebingen 72076, Germany
Location/Qualifiers
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1696 GAGATCTCCTCATGACCATGAAGATCCTGGTGACAGGGGGTGCCGGCTTCATCGCCTCC 1755
                                                                                                                                               2353
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                                                                                                                                                                                                                                                                                                                  ACGACGACATCGTGCACTTCGCGGCCGAGTCGCACGTCGACCGCTCCAT---CACCGACA 3617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCGCTGTTCGAACAACTTCGGCCCCCACCAGCATCCCGAGAAGCTCATACCGCGCTTCC 3917
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                                                                                                                                                                                                                                                                                                                                                                                                                                GCCACGCCCCCAGGATTTTCGTCCACATCTCCACGGACGAGGTGTACGGCTCCGTCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGACCAGCCTCCTGTCCGGCGCCACCGTTCCCCTCTACGGCGACGGGCGCGCACGTGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCACGACCGGCCTACGCGGTCGACCACAGCAAGATCACCGCGGAACTCGGTTACCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGGTGCCTTCACCCGCACCAACGTGCTGGGCACCCAGGTCCTGCTCGACGCCGCGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGGAGAGATCTACAACATCGGGGGGGGGCGCACCTCGCTGCCAACCTGGAGCTCACGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTTGCTCGCACTGTGCGGGGGGGGCCCGGAGCGCATCGTCCACGTCGAGAACCGCAAGG
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                                                                                                     CCTACGTCCGCCGGCTCCTGTCGCCCGGGGCCCCCGGCGCGCGTCGCGGTGACCGTCCTCG
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10210. 11784
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RVPHVELAGEGGTVTTTALLRPGRAVLIGLSGDPLRGARLRAATPWFPRVTVTLAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCAPALGAELGGYGNVORLFADLEAELTDRTGRADLDILVNGADDVOGVAPERATPE
EFDRLVAAGAKAPYEVIQRALRSLADGGRVINISRGAVEPVEPKAVAYAMAKGAVETL
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                                                                                 AVRRLSGIAFPGEDASRELIRADVAGIDIPPRRFQRLESGLAIAARRPDGVTRVMVHE
                                                                                                                                                                                                   VDHSAPLADVDAVLARPDGHVVWTGSAGEAELHAVLRRWFGEPEPAGTAGTRFRAHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MTHAGGGAGRAAAMRLAAAGALVAIHHTGDEQAADDVVRAIGEG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAGGTGAAGGCCCTGGTCCTGGCAGGTGGAACCGGCAGCAGACTGAGGCCGTTCACCCA 2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2324 CACCGCCGCCAAGCAGCTGCTCCCCATCGCCAACAAGCCCGTGCTCTTCTACGCCGCTGGA 2383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Gaps
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Best Local Similarity 65.3%; Pred. No. 7.2e-58;
Matches 1325; Conservative 0; Mismatches 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="decarboxylase homolog'
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9626. .10207
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                                                                                                                                                                                                                                               8803. .9471
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8803. .9471
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                                                                                                                                                                                                                                                                                                                                                  'note="LanN"
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KHGVPGFRALGHTATGTTTVAN VCPGY VPTPMAQRVRGGYAAAX NATEDA ILEKFQ
AK I PLGRYSTPEEVAGLVGYLASDTAASITSQALNVCGGLGNF"
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IIEPLAADESRIRLLHDYRAIDDDPDSLKWIDEAVDRNSRSELAALKTNVELAHATEE
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GHTHTTKFYRVCFSHQKIAYKQVTLPALMTLHTGYWTFTENEDGVTASSQHTVVLNTE
RTPISSIKSMYGHSLGAIGSIEIAASLLAMENHVVPPTANLHTPDPECDLDYVPLVAR
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                                                                                                                                                                                                                                                                                                                                                                 SDQAGGLDA IAQARRO IRKGSKLICSGGVDASICPWGWVAQLANGRYSTSENFERAY.
PFDADASGYVPGEGGALLILEDAEAARQRGAENVYGEIAGYGSTFDPRPGSGREPRLR
FAIELALADADAEPSDIGVVFADAAGTPELDRVEAEALIEVFGAAGVPVTAPKINGR
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GGFNSAMVVRGTDR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="acyl carrier protein homolog"
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transl_table=11
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1855, .5075
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gene="lanL"
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gene="lanD"
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gene="lanc
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                                                      12502 TGCCTTCGGGGTCGCCGAGCTGGCCGCGGACGAGGCCGAGGCCCTGGTGGAGAAGCC
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomycineae; Streptomycetales; Streptomycineae; Streptomycetales; Streptomycineae; Streptomycetales; Streptomyces.

I (bases 1 to 5010)

Blubb, M.J.

Direct Submission

L Submitted (29-AUG-1996) M.J. Bibb, John Innes Centre, Norwich Research Park, Colney, Norwich NR4 7UH, UK

Research Park, Colney, Norwich NR4 7UH, UK

Submitted (29-AUG-1996) M.J. Young, P., Postma, P.W. and Bibb, M.J.

Substrate induction and glucose repression of maltose utilization by Streptomyces coelicolor A3(2) is controlled by malk, a member of the laci-galk family of regulatory genes

L Mol. Microbiol. 23 (3), 537-549 (1997)
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FGWRFNLLADGGIINSALDWLHLPTPAMLEDTFWQRFSALWWYWGGVPFWMVSLLGGP
PVIDNSLYBASEMDGANAWQRFRYYTLPGLRSVSSTYVLLGIIWTFNQFAVIFLLFGN
TAPDAQILVTWAYQLGFGQQPRDFAQSAAYGILLLAILLVFTSFYRRWINRNGQLAN
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IDNYFGLILVYCSTAVPYCAMLLKGYFDTIPPEIDEAGRVDGLTPFGTFFRLILPLAR
PGLAVGGFYSFITAFGEVAFASTFMLSDTKYTFAVGLQSFVSEHDAQRNLMAATAVLV
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Best Local Similarity 63.0%; Pred. No. 1.2e-56;
Matches 1683; Conservative 0; Mismatches 800; Indels 188;
                                                                                                                                                                                                                                                    /product="putative maltose permease"
/protein_id="CAA68974.1"
/db_xref="GI:1524335"
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DDRAAMSLATHIVSLCHTRIGLAGPRRPYPVQRKIEGFVRTVQDDLGLSAETVEK
ELVOHSLYTLEGGGAAASALIRDCTAVVCASDWAMGAIRARQLGLDVPRDVSVVG
FDDSPLIAFTDPPLTTVRRPVPAMGQAAVRTLLEEIGGTPAPHSEFVFMPELLVVRGST
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VNAAAAKKGYGTWLSLFDGKGLHKADTTADAYAH IOBAFVSGKVASTIQGPWEITNFY
KGTAFKDKNNIGIATVPAGSTGKAGAPTGGHNLSVYAGSDKAHQEAALKFVNIMTSAK
SQETVALKNSTLPTADAYTAKVKADPGIAGEQTVLPAAQPRPALPEYSSLWTPLDDE
LPQIAGGKKSLDEGLGDAETAIAKLVPDFSK
                                                                                                                                                                                                                                                                                                                                                                                    /traislation="mttrladiaaqagyseatyskylngkpgyaattrosylaaldyl
gyerpyrlrqrseglyglitpelenpirpalaqyiggaltrogytpylatqtpggste
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VVIGDLVLYPLGYGLXLTLTDANSLNSARTIGVNEIEATYKFVGLDNYADILMGPTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'translation="MRGIAATALVASLALAATACGGDGDSDSESGGPVTITYWDTSN
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PAFAKKGFFLPLDGTEALAEQDKFQPNLIEQAKYEGKTYGVPLVTDTLAFVYNKELFE
van Wezel,G.P., White,J., Bibb,M.J. and Postma,P.W.
The malEFG gene cluster of Streptomyces coelicolor A3(2):
Characterization, disruption and transcriptional analysis
Mol. Gen. Genet. 254 (5), 604-608 (1997)
97340948
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Protein_id="CAA68972.1"
/db_xref="GI:1524333"
                                                                                                                                                                                                                                                                                                               transcription"
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/protein_id="CAA68975.1"
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/gene="malR"
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                                                                                                                 Location/Qualifiers
1. .5010
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1525. .2891
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oy Ob	4992	GGGCACCTGCCGCTCGTGCGGCCGTCCGGTCTCGGCGGTGGTGTCCGCGTG 5051	
χς qα	5052 860	CAGTCCGGAGACGAAGATGATGCCGGACACCCCGCGGTCCACGAGCATCTCCGTGAGTTC 5111 	
% a	5112 920	GTCCTCGGTCGACCCCGGGGTCTGCGTGGCGAGCACGCGCGTGTAGCCCTGACGCGT 5171 	
Oy Op	5172 980	GAGCGCCTGCCCCATCACCTGGGCCAGTGCGGGAAGAGGGTTGTCCAGTTCGGGGGT 5231 	
oy Op	5232	GACCAGICCGACCAGCTCGGCGCGCGCTGTCGCGCCGGCTGCTGGTAGCCCAG 5285	
9 9	5286	CGCGTCCAGTGCGGTCACCGAGTCGCGGTGCCGGTGGCCACACCGCGCGCACTT 5345	
Oy Op	5346	CAGCACCGGGTGACGTGGCTGCTGACGCCCGGGCTGCGATGTCGGCGAGCCG 5405 	
\$ 8	5406	CATGGTCATGGCAACGCACTCTACCTGTCGGGGCGTCAGGGCGTGC 5451 	
장 <u>원</u>	5452	CCACCGCGCGCGGAACCGGGGACTGCGGGCCCGTCCGCCGCCCCACGGACCACG 5511	
o d	5512	CGCCCGAAACGATGGCTGAAAATGCTTGCAGCAAATTGCC	
ογ	5552	5551	
g	1400	GGGCCCCGTAAACAAGCGTCTCACGACGGTCGCCGAGGGTCACGCCCGGATAACTTCGG 1459	
\$ a	5552 1460		
Oy Op	5590	CTGGCAACCCCGGCGCCGCAGAAGCGGTTGGCGTGAGGCGTCC 5634	
60 61	5635	AGACCTCGGCCGATTCCGGGATCACTCAGAGGGGTTCACAATGCGGCGTGGCATTGCGG 5694	
o o	5695	CCACCGCGCTGTTCGCGGCTGTGGCCATGACGGCATCGGCGTGTGGCGGGGGGGCGACAACG 5754	
Oy Dp	5755 1699	GCGGAAGCGGTACCGACGGGCGCGCACGGAGCTGTCGGGACCGTCACCTTCTGGGACA 5814	
ري اور اور	5815	CGTCCAACGAAGCCGAGAAGGCGAGGTACCAGGCCCTCGCGGAGGCTTCGAGAAGG 5871	
, 9 9	5872	AGCACCGAAGGTCGACGTCAAGTACGTCCCGTTCGGCGAGGCGAACGCCAAGT 5931	

6408 2577 6753 6348 6522 6580 6633 6693 2638 CCCTGAAGAACTCCACGCTGCCGACGCCCTAC---ACCGCGAAGGTCAAGG 2694 5991 6051 6108 2040 6168 6228 6288 2217 6462 2397 2457 2517 6754 ACAACGAGATGGTGAAGTTCTTCAAGCCGGCCGTCGACAAGGCCGTCGAACGGCCGTGGA 6813 2041 acescerecerecereceacacecrecerrecereacaacaacaacaacaacaacaacaacaa 2100 2101 AGGCCGCGCTCGAGGCCCCCAAGACCTGGGACGTGAAGAAGGCCGCCGCCACCGTCA 2160 2278 ACGCCGCGGGCCAAGAAGGGCTACGGCACGGCTGAGGCCTCTTCGACGGCAAGGGCC 2337 2578 AGGAGGCGCCCTGAAGTTCGTGAACTTCATGACCTCGGCGAAGTCCCAGGAGACCGTCG 2637 6349 ACGACGAGCGGTGCGCGCTACCGCGTCATCAAGGACCTCGTGGACGCAGCCGG CCTACCTCTACGGGGGGGGGGGGGGCGTCGTCGACGAGAAGAACAAGACCGTCACGGTCG 6463 GCAAGGTCGCCATGATGGTCAACGGCCCTGGGCCATCGAGGACGTCAAGGCGGGAGCCC 2338 GCAAGGTCGCCTCGATCATCCAGGGCCCGTGGGAGATCACCAACTTCTACAAGGGCACGG 6634 TCGACGCCTCCTACGCCTTCGTGAAGTACATGAGCTCCGCCAAGGTGCAGCAGCAGACCA 6409 CCATCACCGACG -----CGTCCGACGCTGGAACAACATGCAGAACGCCTTCAAGTCGG ACGCGGTCCCGCAGGTGATCGACCCTGGCGCTCTTCTACAACAAGGAACTGCTGACGA AGGCCGGTGTCGAGGTGCCGGGCTCCCTCGCCGAGCTGAAGACGGCCGCCGCCGAGATCA CCGAGAAGACCGGCGGGGGGCGTCTACTGCGGGGGGGACGACCCGTACTTGGTTCCTGC TCAAGAACGCCGCGGCGCCAACTCCGGTGCCCCGGACGTGATGCGTACGGAGGTCGCCT GGGTCGCGGACTTCGCCAGCATCGGCTACCTCGCCCCGCTCGACGGCACGCCCCGCCTCG 6814 TCGCCGAGGCAATGCCCTCTTCGAGCCGAT 6844 2755 1921 6229 6889 6109 6919 5932 5992 g 셤 à g ò g δ q ð q à a ò g ò g qq g g g QQ ð 엄 ŏ à a ò ò à ò å

RESULT 12 SC10B7/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS

SC10B7 33517 bp DNA linear BCT 12-MAY-2002 Streptomyces coelicolor cosmid 10B7.
AL355752 AL645882
AL355752.2 GI:20520696
acctyltransferase: alpha-glucosidase; arsC; bi-functional protein (secreted alpha-amylase/dextrinase); carboxylesterase; glnE; glnII;

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RBS
gene
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integral membrane protein; iron-sulfur oxidoreductase; lipoprotein; malE; malE; malG; malR; reductase; regulatory protein; secreted protein; tetR-family transcriptional regulator; transcriptional regulator; two-component system response regulator; two-component system sensor kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-MAY-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk RR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 33517)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Redenbach, M., Kleser, H. M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.

Kinashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
97000351
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Cerdeno, A. M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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/note="SC02207"
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Seeger, K.J. and Harris, D.
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Anote="SCIOB7.05, glnII, glutamine synthetase, len: 343 aa; identical to previously sequenced TR:09x958 (EMBL:Y13833) Streptomyces coelicolor glutamine synthetase
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AQRNCMHPTDYRAL-"ALMDARAGEATTAGH.GAALGI.NSAGTTALVDRLERAGHVRR
VRDERDRRRVTVEVDERAVALGWSHFGPLIGRAVELLRGYDERELAAIRGFLTGVREA
AADDGREPRHNEPG"
/note="SC10B7.02, hypothetical secreted protein, len: 231 asi identical to previously sequenced TR:03X555 (EMEL:113833) Streptomyces coelicolor hypothetical 23.4 kb protein precursor. Contains a possible N-terminal region
                                                                                                                                                                                                                                                                                                                                            /product="hypothetical secreted protein"
/protein_id="CAB90855.1"
/protein_id="CAB90855.1"
/db_xref="61:7799232"
/db_xref="e1" sPTREND:.QP55"
/tb_xref=tion="MSRRFIGTOKKIVLLVGAAAVAGGGAFLAATASNAAQTTPEAR
TKAAQDSGVCQGLATALGNNORFIEGORADPDAQSQARIENREAVVAEIERKQAASGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVGESAQDPQÄAQPPQSGQDTGGQAGDQAGDQAGNQTGDRAGGAAQAGEQVCÄGSTVT
LSGEGGAPAASSDRFPVGTKLRVTNLDNDKSTTVEVNSVSGSCALLNNAAFEQVREEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1771. .2043)
/gene="SC10B7.03c"
/gene="SC10B7.03c"
/note="SC10B7.03c"
/note="S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor putative marR-family transcriptional regulator, SCF43A.30c, 168 aa; fasta scores: opt: 276 z-score: 336.5 E(): 2.3e-11; 39.9% identity in 153 aa overlap"
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/protein_id-"CAB90857.1"
/db_xref="GI:7799234"
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/gene="SC10B7.05"
/note="SCC2210; glnII"
2816. .3847
                                                                                                                                                                                                     signal peptide sequence'
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/gene="SC10B7.03c"
/note="SC02208"
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/qene="SC10B7.04"
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/note="SC02209"
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/gene="SC10B7.05"
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/transl_table=11
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(EC 6.3.1.2) (glutamate-ammonia ligase) GlnII, 343 aa and highly similar to SW:GLNZ_STRVR (EMEL:X52842) Streptomyces viridochromogenes glutamine synthetase II (EC 6.3.1.2) (glutamate-ammonia ligase II) GlnII, 343 aa; fasta socres: opt: 2196 z-score: 2572.0 E(): 0; 91.0% identity in 343 ao overlap. Contains Pfam match to entry PF00120 gln-synt, Glutamine synthetase and two matches to Prosite entries PS00180 Glutamine synthetase signature and PS00181 Glutamine synthetase signature and ps00181 signature.
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/translation="MEIDGYLPLRYETENGOSHARIRAAELRELVLRIGHAGDHFLVV
                                                                                                                                                                                                                                     /traislation="Wifkaetividgteptakirsktkiitaapagidatpvwgfdgs
Stnoaegsssdcvlkpvfscpdpirggediivilcevidtowsphpswyraalaeiser
Praoepverie tedytfergtraicfpredgeptaggsyrgggsyrggsgeterbuvveahlen
Clkacigisginaevwpcgweegvgplapleysdgiwyarmilytraedfergatldp
KPVKODWNGAGAHTPSTKAANEGYDAIITAAESLGEGSKPMDHVKNYGAGIDDRLTG
LHETAPWNEYSYGVSDRGASVRIPWQVEKDGKGYIEDRRPNANVDPYVVTRLLVDTCC
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//gene="SC10B7.05"
//octe="F20L0B7.05"
//octe="F20L0B7.05"
//gene="SC10B7.05"
//gene="SC10B7.05"
//gene="SC10B7.05"
//note="F200180 Glutamine synthetase signature 1"
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Pred. No. 6e-57;
0; Mismatches 800; Indels 188;
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/note="SC10B7.06, unknown, len: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"hypothetical protein
/protein_id-"cab90859.1"
/db_xref-"GI:7799236"
                                                                                                                                                                             /product-"glutamine synthetase"
/protein_id-"cAB908888.1"
/db_xref="gl:7799235"
/db_xref="SPTREMBL:Q9X958"
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/gene="SC10B7.05"
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/note="SC02211"
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                                                                                                                                               19576 GGGCACGCCTGCGCGCAGCCGCTGTAGCGCTGCATGTCGGCGGTGGTGTCGGCGTG
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                                                                            GTGCTGCACGAGCTCCTCGGACTCCCGC ---GCCGACACTCCCAGGTGCTCCCGCACGCC
                                                                                                                                                                                                     GCCGACGCGCTCGTGCCCCCAGCTCCGCCAGGTGCGCCAACGCCCAGGCGCATCGCGGCCCCG
                                                                                                                                                                                                                                                                                                               GTCGTCCGGGGAGGAGGGTGCCTCGATCCGGGGCGAGAACCCGTTCACGAGGACGAA
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CCGGCGCGCGCGCACGCCCGAGGGCCATCATGTCGCTGGCGCACATGACGGCGGT
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                                                             GCAGCCCAGGTCGATCAGCGCGGACGCGGCGGCCTGGCCCCCCTCCAGGGAGAACAGCGA
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                                                                             GGGTCGCGGACTTCGCCAGCATCGGCTACCTCGCCCCGCTCGACGGCACGCCCCGCCCTCG
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                              AGACCTCCGCCCGATTCCGGGATCACTCAGGGGAGTTCACAATGCGGCGTGGCATTGCGG
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acyl carrier profein; aromatase;

CDP-4-keto-6-deoxyglucose-3-dehydratase(El); cyclase;

CDP-4-keto-6-deoxyglucose-3-dehydratase;

dTDP-1-glucose synthase; disulphide bond-forming protein;

dTDP-1-glucose synthase;

dTDP-1-glucose-4,6-dehydratase;

dTDP-1-glucose-4,6-dehydratase;

dTDP-3-glucose-4,3-dehydratase;

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biosynthetic gene
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Tu22 genes involved in
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Norfolk NR4 7UH, U.K
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Streptomyces violaceoruber
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Sherman, D. H., Malpartida, F., Bibb, M.J., Kieser, H.M., Bibb, M.J.
Hopwood, D.A.
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AGGAGGCGCCCTGAAGTTCGTGAACTTCATGACCTCGGCGAAGTCCCAGGAGACCGTCG
                                                                                                                                                                      ACAACGAGATGGTGAAGTTCTTCAAGCCGGCCGTCGACAAGGCCGTCGAACGGCCGTGGA
                                                                                                              J. (Dases 1 to 39250)
Ichinose, K., Bedford, D.J., Tornus, D., Bechthold, A., Bibb, Revill, W.P., Floss, H.G. and Hopwod, D.A.
The granaticin biosynthetic gene cluster of Streptomyces violaceoruber Tu22: sequence analysis and expression in a
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/strain="Tu22"
/db_wref="taxon:1935"
complement(1099. .2417)
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granaticin
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Direct Submission
Submitted (22-SEP-1998) Hopwood D.A.,
Norwich Research Park Colney Norwich,
Location/Qualifiers
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99051446
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us-09-922-683-7.rge

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/translation-"mtgeavylvsgrgvravrgapaealaplldgtrtpdevlreaar.
ardarrplergvrralaelwsagllrahpdpaatpgtgagppaahdrsaeafwdlagt
tppartavrllvldgpvseeearaacaasgldvgrpgagasdaevtlvlctdyldprl
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DGSGYTVDDPHALSWWRTATVAGQPHLLPDPQRAPSRPGSWTYTARADLSEDVAALAA
LADERGLEVLVLDQTRPDIGLPVVKVVVPGMRQFWPRFAPGRLFDVPVALGRLAEPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mnsreqofdeldssasylshedsdlpaprlartyllaamagysl
vtvvnilgaglspaetcvgftallvvfglqvahsrpqarqspywrrytillqavfcf
vplalfhmawgamggflagsvllllpgraamplygaigaslfaysaaaghtllbsvyt
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LEAAGTEVEAAIDIGPLPSQIDTVLATVLREGVTNALRHSRVHHCTIRCWEKDGVVTL
SLGNDGVDPEDGGYEGVDRDARRADDPGGTGLGNLTYRLTRVGGSLTTELSDNGWFRM
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LGCTSPVARPDASLAASRAAGLHTAVLETAKWLAGVPGPTRDAVHTVDALTLDSARHP
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LCEAVERYSGSRHGDEPVVRDSFRAFGPAAVHPDTVRLYDPRQLRDRDAWNASGSPFQ
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kyrpyvalidiglegiediraalliaeeleschrilifisterpevlrraldakyagfi
pkdaspodlaeavrilaaghra idpolalaamdsasselterrmevlrkilaegdeape
iaarlhistgtvrnyllsvvtkinarnrvdavriahesgwly"
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                                                                                                                                                            /product="putative two-component response regulator"
/protein_id="CAA09631.1"
/db_xref="GI:4218542"
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/gene="gra-orf12"
/note="putative terminator (stem 8 bp, loop 8 bp)"
complement(6716..8971)
/gene="gra-orf12"
/function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative two-component sensory kinase"
/protein_id="CAA09632.1"
/db_xref="GI:4218543"
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/gene="gra-orf11"
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/db_xref="GI:4218544"
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/gene="gra-orf12"
complement(9059. .9245)
/gene="gra-orf13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="gra-orf11"
/note="2 CC/CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5051, .5140)
/gene="gra-orf10"
/note="4 CC/AA repeats"
/bound_molety="SARP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6688. .8981)
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                 /gene="gra-orf10"
/codon at=-
                                                                                                                                                                                                                                                                                                                                                                                               complement (5036. .5038)
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complement (5051. .5140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(5125, .6345)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "SARP"
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                                                                                                                                   /transl_table-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /bound_moiety
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/gene="gra-orf9/gra-orf10"
/gene="gra-orf9/gra-orf10"
/gene="putative bidirectional terminator (stem 12 bp, loop 9 bp)"
complement(join(4418. .5038,5051. .5140))
                                                                                                                                                                                                                                                                                                                                                               LITETNIVVOGTECTRAEEQMICAEDDEPADLEAVGILALILGERKDERALIETELINGER CORPEGAPOR OF THE CONTROL OF THE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STCFGGYRLALRPEDSDLREFQSLARGSVALEAGDARAASAALERALGLWRGTALVD
VPVGRVLGVEVLGMEEQRTRVLEQRIEADLLLGRHASLLAELRMLVARHPMNENLAAQ
LMTALYRSGGVWRALEVFQELRRTLIEELGVEPSHRLQLLHRAVLSGELELDPRHAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MDVGILGPLAVRLNGQSIVPSAGKPRQLLALLAIRAERVVTVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMEEIWGDAIPKSAATTLQTYILHLRRKVTAALRAGQPGAAADRAGTGAGAGDAKSVL
                                                                                                                                                                                                                                                                              /translation-"MGEVFAGRYELIDPIGRGGVGAVWRAWDHRRRRYVAAKVLQQSD
                                                                                                                                                                                                                                                                                                              ÄHTLLREVREQALRIDHPHVLAPASWAADDDKVLFTWDLVAGGSLAHVIGDYGPLPR
FVCTLLDQLLSGLAAVHAEGVVHRDIKPANILLDVTGTGRPHLRLSDFGISWRKGEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"pathway-specific transcriptional activator"
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complement(3290, .3346)
/gene="gra-orf8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="CAA09629.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(2474. .3022)
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/function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3028. .3031)
/gene="gra-orf8"
3152. .3226
                                       .2400)
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'bound_molety-"SARP"
                                                                                                                                                                                                                                          db_xref="GI:4218539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ______3226
/gene="tRNA-ala"
3152. 3226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232. .3267
gene="tRNA ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232. .3267
gene="tRNA ala"
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/gene="gra-orf9"
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complement(1099.
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'trans1_table=11
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gene="tRNA-ala"
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                                       CDS
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T'n

14154 14394 GGCGGCTCATCGGGGACCATACGCAGGCGGAGGTGGCGGCAT-----GAGGCTCCT 13980 14274 3702 14454 14694 4182 3762 CCACCAGCATCCCGAGAGCTCATACCGCGCTTCCTGACCAGCCTCCTGTCCGGCGGCAC 3942 GCCCGACACCGCGAAGTGGTACGAGCGGCACGAGGACTGGTGGCGTCCCCTGCTCGCC 4300 CCTGCTGCCCAACTCCCCCTACGCGGCGTCCAAGGCCTCCACGACCTGGTCCGCCCCC CATGGGCACCAGCAGCAGCTCGACGCCGCACTCCACGCCGGTGTGGACCGAGTCCTGCA 14215 CGCCGAGTCCCACGTGGACCGCTCCCTCACCGGCGCCCGGCGAGTTCGTCCCTACGAACGT CCACCACGCACCCACGCCTGGACGTCCGGGTGACCCGCTGTTCGAACAACTTCGGCCC TACCACCGTACGCCACGGACTCGCACTCACCCGCTGCTCCAACAACTACGGCCC CGTTCCCCTCTACGGCGACGGGGGCACGTGCGCGGCACGGCTGCACGACGACCACGT CGGCACCTCGCTGCCCAACCTGGAGCTCACGCACCGGTTGCTCGCACTGTGCGGCGCGGG --CCGGGGCCCCCGGCGCGTCGCGGTGACCGTCCTCGACAAACTCACCTACGCCGGCAG CCTCGCCCGCCTGCACGCGGTGCGTGACCATCCCGGCCTCACCTTCGTCCAGGGCGACGT CGTCTCCACCGACGAGGTGTACGGCTCCCTCCCGCACGGGGCCCGCGGGGGGAGAGCGACCC CCTGCTTCCGACCTCGCCGTACGCGCGTCGAAGGCGGCCTCGGACCTCATGGCGCTCGC CAGGGCCGTCGAACTCGTCCGCGTGTCGGGCCGGCCGGGAGAGATCTACAACATCGGGGG CCCGGAGCGCATCGTCCACGTCGAAACCGCAAGGGGCACGACCGGCGCTACGCGGTCGA GTGCGACACCGCGCTCGTCGACACGCTGGCCGCGCGCACGACGACATCGTGCACTTCGC GGCCGAGTCGCACGTCGACCGCTCCATCACCGACAGCGGTGCCTTCACCCGCACCAACGT GCTGGGCACCCAGGTCCTGCTCGACGCCGCGCTCCGCCACGGTGTGCGCACCTTCGTGCA CGTCACCGGCGGAGCGGGCTTCATTCGCTCCGCCTACGTCCGCCGGCTCCTGTCGC-

KEYWORDS

SOURCE

VERSION

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LGTQTLLDAVLDSGVERVVHVSTDEVYGSIEQGSWTEDWPLQPNSPYAASKACSDLVA
RAYCAPTEVDLSITRCSNNYGPHQHPEKVIPRFVTKLLEGRQVPLYGDGRNYREWLHV
EDHCRGIHLVLNKGQAGEIYNIGGGNEYTNLALTEKLLELTGAGPEMIRRVPDRKAHD
LRYSIDESKIREKLGYAPRISFEGGLSDTVAWYRDNPDWWKSIEHGGDSAAA"
2927 c 2638 g 1187 t
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GVTRAGVIVGNRGPEISAVLGDGAEFGMRYTYIPODAPRGIAHTVATIRDFLCDDDFV
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DPREDMALVGYYFFTAAIHDAVAAIEPSARGELEITDAIGWLVSSGADVRASOYDGYW
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LRHGPLVRSALCAASLNGAYLGLLLJVTYQLHTGPGWNSWQTAVALLPACVPLMVSLP
SAGRWYGRLGAARLIVSGTLAATLGCACCAVWGVSGSYATGALPALLLVBAGFVLSFA
ALNMQAVAGTAPESRQTAVSLYQTAVQLGAALTLPAVALLLGSGGEGFYRTALLLITA
VAAVGAAVACTGTRRKAEQPCVSRR"
4195. . 4803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVSKRHTLRGIHSVSIPPGGAKLVTCVRGALRDIVVDLRIGSPAFGAHOVTELJAVSG
RSVYVPEVWGTDSSRSPTTPVSATSSPSTYVPGTQIDINPLDPDLDLPWDCPQEPLIS
EKDAKASSLAEALASGTLPDLHDCRTSDAARTALVRAPSERG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MNILVTGAAGFIGSHFVRSLLADTYSGWEGARVTALDKLTYAGN
RNNLPPSNPRLEFVRGDVCDRALLRELLPGHHAVVHFAAESHVDRSLEGAGEFFRTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="glycosyl transferase"
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MSYVAPLLALHLGVPHARQTWDAVDADGIHPGADAELRPELSELGLERLPAPDLFIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPPSLRPANAAPARMMRHVATSRQCPLEPWMYTRDTRQRVLVTSGSRVAKESYDRNFD
FLRGLAKDLVRWDVELIVAAPDTVAEALRAEVPQARVGWTPLDVVAPTCDLLVHHAGG
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VALPAIGGDLGLSPQDAQWMMSGFALGFAALLLSGPRITARWGRRRAYLVALLVFAVA
SSAGGLVHSGELLVLTRVIKGMCAALTAPTGLAIIATAYRQGDEQRRAVAVYSFFGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSIPGAFLITPDQLSDERGAFYELRCDMLERAVGVPFQPQQINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTVVQDSHVGPHASIGRRCTVTDSRVENSIALDEASVTGVRGLRNSLIGRSASVGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="GNDP-glucose 4,6-dehydratase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
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/transl_table=11
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4846. .5943
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/gene="urdz1"
4195. .4803
/gene="urdz1"
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5968 . .7035
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/gene="urdH"
7032. .8018
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/gene="urdH"
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2945. 4198
4945. 4198
79ene-"und12"
/9ene-"und12"
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TESRAKMTUTPSYEMELLHERGLVERGPPPDAGPGHEGGIPLDLTARGOW
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GCDGEDSAVRRLAGFAFLGADPTKELLRADLAGIELRERRFERHPNGVANARRGPGGI
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GRVLLAGDAAHVQLPVGGQALNLGLQDAMDLGGKLAAHITGKAGEELLDTTEPATRWR
PAYSATSKHKPSCCSADPMWSLRAVFGELLGLGAARRHLASMISGLDGGAPTSVPRTG
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SYRVTFPHHRIAYKQVTLPALMTLHTGYWTFTENESGTAASSQHTVVLNTENIAGILG
PEATVADAREFIRGALSTNSRATLGHAKDYAENKR"
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NAGVMGGVAPEEVTPELFDRLVAVNAKAPFFIVQRAVTLIPDGGRIINISSGLTRFAN
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DSSRIRLLHDYRAVDDDPQGLKWIDEAVDRNSRSELAALKTNVELAHASEEITFSFED
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                                                                                                                                   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 8018)
Faust, B., Hoffmelster, D., Weitnauer, G., Westrich, L., Haag, S., Schneider, P., Decker, H., Kunzel, E., Rohr, J. and Bechthold, A. Two new tailoring enzymes, a glycosyltransferase and an oxygenase, involved in blosyntheasis of the angucycline antibiotic urdamycin A in Streptomyces fradlae Tu2717
                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 8018)
Faust, B., Westilch, L. and Bechthold, A.
Puret, Submission
Submitted (02-JUL-1999) Pharmazeutische Biologie, Universitaet
Tuebingen, Auf der Morgenstelle 8, Tuebingen 72076, Germany
Location/Qualifiers
                                                     Streptomyces fradiae.
Streptomyces fradiae
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Best Local Similarity 65.0%;
Matches 1306; Conservative
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DTGSPDDLLDCNRVLLGRLRPGVHGEVDAASTVEGTVVVVEAGRSWSDSRLVGPLVVGA
GSVVRGSELGPYTALGRDCYLEDAGIRDSIVLDGVSI QGVRGLSGSLI GRSAAVRTGE
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ITPNPAYNKEVKNVALQFKLPAGAKVLSYEVADRLAAGTPELQIDGTKAVLRAAGPYV
ANAPEDLPKITIKLKAPTTRGTLETPFGGTSHDDPGFTWTFISPNWTARPSSPAGPTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGTOOLLDAALHAGYDRYLHVSTDEVYGSLDSGTWTEDSPLLPNSPYAASKASTTWSA
APTTVRHGLDVRITRCSNNYGPROHPEKLIPNFVTRLLTGRQVPLYGDGRNVREWLHV
DDHCRALQLVLTKGRAGEIYNIGGGSGMSNREMTARLLDLLGADWDWVRHVEDRLGHD
                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases i to 7365)
Bechthold.A., Sohng.J.K., Smith.T.M., Chu.X. and Floss, H.G.
Identification of Streptomyces violaceoruber Tu22 genes involved in the biosynthesis of granaticin
Mol. Gen. Genet. 248 (5), 610-620 (1995)
7476861
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YLGDNILAEGIAESARAFRDERSAARLLLTKVADPRAYGVAETDATGRVHALVEKPER
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                     complete
                                                                                                                                      Streptomyces violaceoruber (clone poJ446-22-24, strain Tu22) DNA
Streptomyces violaceoruber Tu22 dTDP-glucose dehydrtatase (graE) gene, complete cds, dTDP-glucose synthetase (graD) gene, complete cds, ORF4 (Streptomyces coelicolor mar homolog), complete cds.
                                                                                                  dTDP-D-glucose 4,6-dehydratase; dTDP-glucose synthase; transport
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                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .7365
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complement(3279. .4952)
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complement(889. .1854)
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complement(151. .816)
/note="ORF1; putative"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:1935"
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                                                                                                                                                               Streptomyces violaceoruber
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VAGRIARPYTRTGRYKAVLLSGLVLMYVATFWRGVLTADTSLWQTGVAAGWGFGIG
LCWQVMLIATQTGVAPQYRAGAGGGSTFRQIGGTGRHRVFLSMFFRGVERVAAYR
GAASDPATAAVNDFATGQAANKVLGAGRRRYGLDNSSFLDHADPRLAKPFLEGLAA
AMQTVFVVSGVMLLIALVLAAVPKEKPPRAGRRRFGCRRKETGKQPAAKK"
                                                                                                                              IISAALRTIADDLNGISBOANANTSYNITSYIMTALYGKLSDIYGRRPYYCTAVGVFV
LGSVLCGLAQSMTTLAVFRGQCIGAGGLMSLAFAILTDLVPLAERSRYQAWFGAVFGV
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S. glaucescens Hst Pyrococcus abyssi Thermus caldophilu

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S. glaucescens PstI DNA fragment containing acarbose biosynthesis genes.
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           GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                       CTGCAGGGTTCCCTGGTGCACGACCCGCCCTGGTCGACGACCAGGGCGCTGTCGCAGAT
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of
                                                                                                                                                                                           Recombinant DNA molecule comprising genes for biosynthesis acarbose - an alpha-amylase inhibitor useful in treatment o
                                                                                                                                                                                                                                                                              Sequence 6854 BP; 1018 A; 2445 C; 2445 G; 946 T; 0 other;
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           /note= "acarbose biosynthesis
complement (4380..5414)
                                                                     biosynthesis
                                                                                                                                                                                                                                                                                           100.0%; Score 6854; 100.0%; Pred. No. 0; 1ve 0; Mismatches
                                                                                                                                                                        WPI; 1998-033827/04.
P-PSDB; AAW23831; AAW40381; AAW40382.
                                                                                                                                                                                                                         Claim 4; Page 14-28; 35pp; German.
                                         "acarbose
                                                                     'note= "acarbose
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/*tag= d
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5676..6854
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Matches 6854; Conservative
                                                                                                                                           (FARH ) HOECHST AG
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                                CGTGCAGCGGAGGTGGGGGGTCATGATGCCGGTCAGCATCTTGATCGTGGTCGACTT
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δ	1561		•	δδ	2641
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ζο d	1621	GCGCCGGTCGCCTGGACGACCCGCGCGCGCTCGACCACCTCCGCGCCGGTGGAGAG		g g	2701
9 8	1791	GUGGCGCCGGTGGACCCCGCAGGCCGCCCCCCCCCCCCCC		Qy	2761
<u></u> 8	1681	AAGGCGTAGGTGTCGAGCTGTTCGGGCAGCAGCTGGCGAGCAGTTCCAGCAGCCGGCG 1740 	,	qa	2761
8	1741	CGGTCCGGCGTGTTGTTGTTGTACTTTCACACTTTCACACTTTCGGTTGTTTAATCTTCACTTTGGTTTAATCTTTGTTTAATCTTTGGTTTAATCTTTGGTTTAATCTTTTAATCTTTTTAATCTTTTTAATCTTTTTTT		λο.	2821
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δ	1801		:	ολ	2881
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y g	1921	CGTCCGTGGACGGCTTCCTCGAGGCGCCCGGCGCCAGGTGGCGGCCTCCCGTGCCAGG		7 A	3001
3 8	1961	CGICCGIGGGCCITCCTCGGAGGCGCCCGGCGCCCAGGTGGCGGGCCTCCCGTGCCAGGTGCCGGGCCTCCCGTGCCAGGTGCCAGGTGCCAGGTGCCAGGTGCCAGGTGCCAGGTGCCAGGTGCAGGTCAGGTGAGGTGA		δλ	3061
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급	2041			g	3121
ò	2101	TTGAACACACACGCTGCAAGAGTTTGCGGGTTTGTTTCAGAAAAGTTGTTTACGAGCCGCCC		Qy	3181
; සු	2101			අ	3181
ô	2161	CGGCACTCTGGTTGAGTCGACGTGCTTACGGCGCCACGCCTCACGTTCGAGGAA	-	ΟŊ	3241
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ò	2221	CCTGTGAGAACAAGACCGCAGACCGACCGACCTCTCC		Qγ	3301
; <u>a</u>	2221	CCTGTGAGAACAAGCCGCGAGACCGGCTCCCGCGGAGGCCGAGGTGAAGGCCCTGG		අු	3301
ò	2281	TCCTGGCAGGTGGAAACCGGCAGCAGCAGGACGCCGTTTCACCACACACGCCAACACCAACACAACACCAAAACCAAAAACCAAAAAA		Qy	3361
. a	2281			đ	3361
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à	2401	GTGTCCGGGAGGCCGCGTCGTCGTGGGCGCGTACGGCCGGGAGATCCGCGAACTCACCG		δλ	3481
ප්	2401	GEGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGAACCGGGAACTCACCG	-	đ	3481
ô	2461	GCGACGGCATTCGGGTTTACGCATCACCTTCACCTCCACCAGCCCCGCGTTCGGTTC		QY	3541
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검	2521	TCGCGCACGCGGTGCCCATCGCCCGCGGCTTCCTGGGCGACGACGACTTCCTGCTGTACC		q	3601
ò	2581			οy	3661
•			_	q	3661

	QQ	2581	TGGGGGACAACTACCTGCCCCAGGGCGTCACCGACTTCGCCCGCC	2640
	δλ	2641	CCGCGGCGCCCGGCTGCTCACCCCGGTCGCGGACCCGTCCGCCTTCGGCGTCGCGG	2700
	qq	2641	CGCGCCGGCCCGGCTGCTCACCCCGGTCGCGGACCCGTCCGCCTTCGGCGTCGCGG	2700
	οy	0	AGGTCGACGCGGACGGGAACGTGCTGCGCTTGGAGGAAAACCCGACGTCCCGCGCAGCT 3	2760
	g	2701	:GACGCGGACGGGAACGTGCTGCGCTTGGAGGAGAAACCCGACGTCCCGCGCGAGCT	2760
	QQ QD	2761	CGCTCGCGCTCATCGGCGTGTACGCCTTCAGCCCGGCCGTCCACGAGCGGTACGGCCC :	2820
	ò	82	ACCCCTCCGCCCGCGGCGAGTCGGAGATCACCCACGCGTGCAGTGGATCGACC	88
	음	83		88
	ò	2881	GGGCCTGCGCGTACGGGCCGACACCACCACGGGCCCTGGCGCGACACCGGCAGCGGG	2940
• • • • • • • • • • • • • • • • • • • •	g	2881	ACCACCCGGCCCTGGCGCGCGCGCGGCGCGG	2940
	φ	2941	AGGACATGCTGGAGGTCAACCGTCACGTCCTGGACGGACTGGAGGCCGCATCGAGGGA :	3000
	qq	2941	SACATGCTGGAGGTCAACGTCACGTCCTGGACGGACTGGAGGGCCGCATCGAGGGGA	3000
	δλ	3001	GATCGTGC	3060
	q	3001	GGTCGACGCGCACACGCTGGTCGGCCGGGTCCGGGTGGCCCGAAGGCGCGCGATCGTGC	3060
	δŏ	3061	GGGGGTCACACGTGGTGGGCCCGGTGGTGATCGGCGGGGGGCCGGTGCTGTCCA	3120
	g	3061	sercacaceregecceeregrearcegecegerecercercacaacreca	3120
	οy	3121	GTGTCGGCCCGTACACCTCCATCGGGGAGGACTGCCGGGTCGAGGACAGCGCCATCGAGT	3180
	qq	3121	3TCGGCCCGTACACCTCCATCGGGGAGGACTGCCGGGTCGAGGACAGCGCCATCGAGT	3180
	οy	3181	ACTCCGTCCTGCTGCGCGGCGCCCAGGTCGAGGGGGGGTCCCGCATCGAGGCGTCCCTCA 3	24
	අ	3181	CICCGICCIGCIGCGCGCGCCCAGGICGAGGGGGGGGTCCCGCAICGAGGCGICCCICA	3240
	οy	3241	STCTCCCGCAGGCTCACCGACTGGTGA	3300
	qq	3241	ceeccececcercarceecceeccccccarcacaecaecrcacaecrearca	
	δλ	3301	3ACCACGACCATCCTCGTCACCGGCGG	3360
	qq	3301	CGGCGACCACAGCAAGGTGTATCTCACCCCATGACCACGACCATCCTCGTCACCGCGG	
	δλ	3361	AGCGGGCTTCATTCGCTCCGCCTACGTCCGCCGGCTCCTGTCGCCCGGGGCCCCCGGGGG	3420
	qq	3361	GGGCTTCATTCGCTCCGCCTACGTCCGCCGGCTCCTGTCGCCCGGGGCCCCCGGCGG	4
	Qy	3421	ACCTACGCGGCAGCCTCGCCCGCCTGCACGC	3480
	qq	3421	GTCGCGGTGACCGTCCTCGACAACTCACCTACGCCGGCAGCCTCGCCCGCC	48
	ογ	3481	SACCATCCCGGCCTCACCTTCGTCCAGGGCGAGGTGTGCGACACCGCGCTCGT	3540
	q	3481	SCGTGACCATCCCGGCCTCACCTTCGTCCAGGGCGACGTGTGTGT	Ś
	٥y	3541	SCGCGCACGACGACATCGTGCACTTCGCGGCCGAGTCGCACGTCGA	3600
	Q O	3541	SACACGCTGGCCGCGCGCGCACGACGACGTGCACTTCGCGGCCGAGTCGCACGTCGA	3600
	ογ	3601	SACAGCGGTGCCTTCACCCGCACCAACGTGCTGGGCACCCAGGTCCT	3660
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	οy	3661	GGTGTGCGCACCTTCGTGCACGTCTCCACCGACGAGGT	3720
	Q	3661	CTCGACGCCGCTCCGCCACGGTGTGTGTTTCGTGCACGTCTCCACCGACGAGGT	3720

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CTGCTTCCG CTGCTTCCC CTGCTTCCC CACCACCGC CACCACCGC CACCACCGC CACCACCGC CACCACCGC CACCACCGC CACCACCGC CACCACCGC CACCACCGC CACCACCGCC CACCACCGC CACCACCGC CACCACCGC CACCACCGCC CACCACCGCC CACCACCGCC CACCACCGCC CACCACCGCC CACCACCGCCC CACCACCGCCC CACCACCGCCC CACCACCGCCCC CCACCACCGCCCCCCCC	5 <u>-5 6-6 6-6 9-</u>	GCCA GCCA GCCA GCCA GCCA GCCA GCCA GCCA	GGTGGC GGTGGC GGTGGCC TGGACC CGCTCA CGCTCA TGGTGCTCA	CCGAGA CCGAGA CCGGAGA CCGGACA CCATCA CCGGCCT CCGACA CCGACA
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GGGCCGGCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGG	CCTGACCAGCCTCCTG	TTGCTC CACGAC CCACGAC CCACGAC CCACGAC CTTTTTTTTTT	CCGGCCGGCACA CCGGCCGGCACA CCGGCCGCCCCC CGCGGCCGCCCCCCCC	3AG 3AG 3CC 3CC 3CC 3CC 3CC 3CC 3CC 3CC
CCCGCA 111111 CCCGCA 3AAGGC 111111 GAAGGC GGTGAC	CTTCC CTTCC CCTTCC CCCCC CCCCC CCCCC CCCCCC	CCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ACCACCGGCCGGCCGGCCGGCCGGCCGGCCGGCCGGCCG	GGCCA HIIII GGCCCC CCGCC CCGCC CCGCC CCGCC CCGCC CGGTGC CGGTGC CGGTGC CGGTGC
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CGGAACC CGGAACC	ACGCGCT ACGCGCT	TCCGGGG TCCGGGG	CACCTGCC 	CCGGAGACC	5 - 5	CTGC		1990	CTGAC	GCAAC		5 5 E	E S	CAACCCC	GGATCACT(GGATCACT(TGTGGCC	36666	990999	SGCGAC 11111 SGCGAC	STACGT
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CCGCACG CCGCACG	GACGGCG GACGGCG		GAGGAC GAGGAC	GTCCGC	CGTGAG	CTGAC	TTCGG	SAGGG	CGTTCA	00000	SCGCA SGAAC	CGGAAC	GATGG	GITACGI	9000900 11111 11111	GCTG	CGGTA	CGGTA	ACGAAGO ACGAAGO	GTCG
1801 TCC 	61 CC 	21 A 21 A	981	041	T 101	161 C	221 A	281	341 0	401	5401 A0 5461 G0 1	5461 G 5521 C	5521 (581	5641 (701	61	5761	5821	88
yc do	•	•		l & f	8 4 4 E	3 6	a v	g & 7	9 6 8	8 %	g &	Db Qy	g ò	음	5 G	δ d	δ δ	В	λο	ò

XX DT 26-SEP-2001 (first entry)		rermentation; Micromonospora	FH Rey Location/Qualifiers FT CDS Complement (1321382) FT /*tag a //*trg // // // // // // // // // // // // //	RBS COMPLEMENT /*tag= b CDS COMPLEMENT /*tag= c	# W	RBS	CDS CDS		FT CDS 62327275 FT /*tag= 1 FT /product= "EvdF" FT RBS 62266229	CDS	FT CDS 83429364 FT /*tag= m //erg= m //product="EvdH" FT RBS 83338336	CDS complement (9463	KBS complement	CDS	FT /partial FT /note= "No start codon" FT CDS complement (1210813022) FT /*tag= s	놨 a	cos	RBS . C
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Ouery Match 12.8%; Score 877.8; DB 22; Length 109519; Best Local Similarity 56.5%; Pred. No. 2e-100; Matches 1892; Conservative 0; Mismatches 1402; Indels 53; G //read-billerand /*tag- bm /product- "EvbB" complement (55125..55128) /*tag- bn complement (55135..56094) /*tag= bo /product= "EvbC" complement (56100..56103) /*tag= bp complement (56184..56813) complement (43799..44866)
/*tag bc bc | Product | "Evrx" complement (45014..45760)
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45969 CGGGTCACGGATGCCTCCAGGATCGACAAATTGACAGCCATCTTTGAAGAAATCCGC 45910

1141 GCTTCCGCCGTCCGGCCACGCC----GAAGGGGAATCCGCTCGCGGTGCCCTTGGA 1196

46029 GCAGCGGTGGCGAGCTGGCCAGACCGGCGAGCAGCCGGCGCAGGGCGGTTCGGGTA 45970

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1081 AGTGGGTTGCTCGCGTACGTCGAGGCGTACGCCCCGGGGTGGCCGCCTCCGGCCTGCGCA 1140

46089 ACGTCGATGCCGGGGTGGTGGCGCCGCCGCCGGCGGTGGCGACGAGGGTCGCG 46030

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46149 GCGAACTGGGATGCCGGGGTTGGGGGTGATGATCCTGGTAGTGGGAC 46090

961 GGGAAGGGGAATTCAGGGGGGGGGAGCGCTCCTGGATGAGCTCGCCGAGGACGCGCACG. 1020

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44621 44261 43841 43721 44860 GCGCTGGTCCTGGCGGGAGGGGTGGGATCGAGATTGCGTCCGATCACCCACACGTCCGCC 44801 2453 44681 44620 CGGGGGCTGGCGCACGCCGTGCTCATCTCCCGCGACTACCTCGGCGACGACGACTTCGTC 44561 44501 44500 CAGGAGCGACCGCACGCAGATCATGCTGACCCGGGTCGCCGACCCGCACGCCTTCGGC 44441 2873 2933 44201 2993 44141 3113 3233 3413 2573 2753 3114 AACTCCAGTGTCGGCCCGTACACCTCCATCGGGGAGGACTGCCGGGTCGAGGACAGCGCC 3173 3293 3353 GCGGCGCGTGTCCGGCAGCCCGGCGTCGTCGTGGCCCGTACGCCCGGGAGATCCGCGAA CTCGGTCTCGCGCACGCGGTGCGCATCGCCGCGGGCTTCCTGGGGCGACGACGACGACTTCCTG GTCGCGGAGGTCGACGCGGACGGGAACGTGCCCTTGGAGGAGAAACCCGACGTCCCG 2754 CGCAGCTCGCTCATCGGCGTGTACGCCTTCAGCCCGGCCGTCCACGAGGCGGTA 2814 CGGGCCATCACCCCTCCGCCGCGGGGGAGCTGGAGATCACCCACGCCGTGCAGGGATG 44320 GCCGAGCTGAAGCCGTCCTGGCGCAACGAGCTGGAGATCACCGACGCGGTGCAGTGCAGTG 2874 ATCGACCGGGCCTGCGCGTACGGGCCGAGACCACCACCGGCCCTGGCGCGACACCGGC 44200 AACCTCGCCGACATGCTGGAGATGAACCGGTTCGTCCTCGGCAGCGTCGAGCCTTTGGTC GAGGGGAAGGTCGACGCGCACAGCACGCTGGTCGGCCGGGTCCGGGTGGCCGAAGGCGCG 3234 TCCCTCATCGGCCGCGGCGCCGTCGTCGGCCCCGCCCCCGTCTCCCGCAGGCTCACCGA CTGGTGATCGGCGACCACAGGAGGTGTATCTCACCCCATGACCACGACCATCCTCGTCA CCGGCGGAGCGGGCTTCATTCGCTCCGCCTACGTCCGCCGGGCTCCTGTCGCCCGGGGCCC AAGCAGCTGCTCCCCATCGCCAACAAGCCCGTGCTCTTCTACGCGCTGGAGTCCCTCGCC GCCGATCCGCGCGCCCGGCTGCTCACCCCGGTCGCGGACCCGTCGGCCTTCGGC 3054 ATCGTGCGGGGTCACACGTGGTGGCCCGGTGGTGATCGGCGCGGGGTGCCGTCGTCAGC 3174 2334 2394 2514 2574 2634 2694 2934 2994 3354 44800 44680 3294 g g & g δ <u>염</u>. δ g g g οy q δy q g g 셤 ò q δ 셤 ŏ g δ d ò g ò ò ò ò ò õ ò

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                                                                                                                                                                                                                                                  3768 TICCGACCICGCCGIACGCGGCGICGAAGGCGGCCTCGGACCICAIGGCGCTCGCCCACC
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CCGGC-----GGCGTCGCGGTGACCGTCCTCGACAAACTCACCTACGCCGGCAGCCTCG
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ABL50555 to ABL50562 represent contigs 1 to 8 from the Micromonospora carbonacea everninomicin biosynthetic locus gene cluster. The contigs encode the protein sequences designated ORF (open reading frame) 1 to 49, given in ABB06881 to ABB06890. The gene cluster is useful for the construction of the everninomicin antibiotic in overproducing strains, and to allow chemical modifications of everninomicin to enhance certain properties via genetic manipulation or combinational biosynthesis. The gene cluster can be used to produce genetic systems and genes encoding novel enzyme activities, and avoid the problems of low yield and quality of everninomicins produced by chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGGCCGCCGATCCCGGGCGGGCCCGGCTGCTCACCCCGGTCGGGGACCCGTCGGC 2687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 817.2; DB 23; Length 14186;
Pred. No. 8.1e-93;
0; Mismatches 723; Indels 15;
                                                                                                                                                                                                                                                                                                      Novel isolated gene cluster encoding polypeptides involved in everninomicin biosynthesis useful for construction of everning overproducing strains, and to allow chemical modifications of everninomicin to enhance certain properties -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14186 BP; 2084 A; 4892 C; 5016 G; 2194 T; 0 other;
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gene cluster; genetic manipulation; contig; gene;
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FARNET C.
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63.7%;
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                                                                                                                     29-JAN-2001; 2001WO-CA00128
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Matches 1296; Conservative
                                Micromonospora carbonacea
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                 Actinoplanes sp. SE50/110 (CBS 614.71) designated acbA, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, R, S, U, V, W, X, Y and Z, and asp3.1, G, H, I, J, K, L, M, N O, P, Q, R, S, U, V, W, X, Y and Z, and asp3.1, and their homologues The products of the invention individually or collectively, are used for synthesis or bioconversion of acarbose (or its precursors or related substances with alpha-glucosidase inhibiting activity), especially of alpha-glucosidase inhibiting activity), especially of alpha-glucosidase inhibiting compounds in Actinoplanes or other organisms. This sequence represents a DNA fragment which encodes the genes involved in the acarbose blosynthesis and bioconversion pathway which are described in the
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                                                                                                                                                                   Score 745; DB 24; Length 38064;
Pred. No. 5.4e-84;
0; Mismatches 370; Indels 3;
                                                                                                                                                 Sequence 38064 BP; 5622 A; 13333 C; 13603 G; 5506 T; 0 other;
     Page 67-77; 80pp; German
                                                                                                                                                                       Query Match 10.9%;
Best Local Similarity 72.4%;
Matches 980; Conservative (
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ACBTDOSE; ACDBASD; ACDBASD; ACDCASD; ACDDASD; ACDEASD; ACDFASD; ACDFASD; ACDHASD; ACDTASD; ASD3-1; ASD3-2; ASD3-3; bloconversion; blosynthesis; alpha-glucosidase inhibitor; ds.
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                                                                                                                                                                                                AGCTGTTCGGGCAGCAGCCTGGCGAGCAGTTCCAGCAGGCCGGCGGCGGTCCGGCGTGGCG
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                                                                                                                                                                                                                    CCGCTGAAGGCCTGGTGGCCGATGTCCCAGTGGACCAGCATCCGGGCGCCCCATGGTCTTG
                 CCGTGGAAGCCGTGGCGCAGGGCGCAGATCCGGTTGCGGCCCGGCGCGCGGCGGTCGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinoplanes sp DNA encoding acarbose synthase AcbVAsp.
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ABA99445/c
ID ABA99445 standard; DNA; 1350
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TCCTCGGAGGCGCCCGGCGCCAGGTGGCGGGCCTCCCGTGCCAGGTGCTGTGTCTGCCGT 1995
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                                                                                                                                                                                                Narbonolide polyketide synthase; PKS; cosmid pKOS023-27; contig 003; ketolide; dNDP glucose synthase; dehydratase; picromycin; narbomycin; antibiotic production; ds.
                                                                                                          119 TCTTCGGAGGCTCCCGGAGCCAGGTGACGCGACTCCCGGGCGAGGCAGGTCGGCCTG
GGGTACTCCAGGCCCAGGGGACAGCGGTAGCCAGTAGGGGCTGTAGCCAGCAGCAGCTGTTG
                                        GGATAGCTCAGCTCCAGCGGGCACCGGTAGCAGTACGGGGCCGTACCCAGCACGCTGTTG
                                                                                   CCGCTGAAGGCCTGGTGGCCGATGTCCCAGTGGACCAGCATCCGGGCGCCCATGGTCTTG
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/note= "glucose-1-phosphate thymidyl transferase"
1114..2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contig 003 from cosmid pKOS023-27 from Streptomyces venezuelae.
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/transl_except= (Pos:2874..2876, aa:Xaa)
/note= "Xaa = Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 CTCACCGGAACCGCCGCCGGTCGCGGGCGCCGGTGTCGAAACGAAC 14
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                                                                                                                                        This invention describes novel nucleic acid sequences from Actinoplanes sp. SESO/10 (CBS 614.71) designated acbA, B, C, D, E, F, G, H, I, J, K, L, M, M, O, P, Q, R, S, U, V, W, X, Y and Z, and asp3.1, 3.2 and 3.3, and their homologues. The products of the invention individually or collectively, are used for synthesis or bioconversion of acarbose (or its precursors or related substances with alpha-glucosidase inhibiting activity), especially of alpha-glucosidase inhibitors. The products can also be used for optimising/inducing production of such compounds in Actinoplanes, or other organisms. This sequence encodes a protein involved in the acarbose biosynthesis and bioconversion pathway which is described in the disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCTCGACGACCTCCAGCGTGGCGCGGGGGGGGGATCCCCCAGTGGGTTGCTCGCGTAC 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     859 TAGACGCCCCGGCCGGTCTCGGGGGGGGGGGGCCGACGGCGTCGGTGACGAACTCC 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.8%; Score 739.6; DB 24; Length 1350; Best Local Similarity 73.4%; Pred. No. 4.2e-83; Matches 959; Conservative 0; Mismatches 344; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1350 BP; 176 A; 503 C; 482 G; 189 T; 0 other;
                                                                                                      Claim 1; Page 10; 80pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  959
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This is contig 003 from the recombinant cosmid pkOSO23-27 DNA sequence (see AA25601) which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of cosmid contains open reading frames which encode the various modules of confensations and subsequence for a narbonolide PKS.

The invention relates to polyketide synthase (PKS). The invention relates to recombinant DNA containing a coding sequence for a narbonolide PKS.

CC series of condensations and subsequent modilications. Modular PKSs are responsible for the production of many antiblotics including picromycin. The narbonolide PKS consists of a loading module, six extender modules.

CC and two thioester domains. Four proteins make up the narbonolide PKS or PICAIII and PICAIV). PICAI includes the loading module of and extender modules I and 2, PICAII includes extender module 6 and atype II thioesterase domain. The second type II thioesterase domain. The second type II thioesterase domain. The second type II thioesterase domain is found on the PICB protein. The nucleotide sequences encoding correquired for this conversion, and the desosaminylated in S. venezuelae to yield narbomycin, the desosaminylated in S. venezuelae to yield narbomycin, and the desosaminal blosynthetic genes are compinant to cosmid pKOSO32-27. Narbonolide is desosaminable to express, in transformed cells, narbonolide (or its derivatives) cor other ketolides (particularly hybrids), which may then be converted cells, by other enzymes recombinantly expressed in the same hosts) to converted to human or veterinary medicine. The nutlein intermediates. The antibiotics are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2329 CCGCCAAGCAGCTGCTCCCCATCGCCAACAAGCCCGTGGTCTTCTACGCGCTGGAGTCCC 2388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.8%; Score 531.6; DB 21; Length 3291;
53.4%; Pred. No. 1.5e-57;
Ive 0; Mismatches 1179; Indels 108;
                                                                                                                                                                                                                                                                                         New recombinant DNA encoding a domain of narbonolide polyketide synthase, for production of ketolide antibiotics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3291 BP; 521 A; 1289 C; 1044 G; 436 T; 1 other;
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                                                                                                                                                                                                     Betlach M, McDaniel
                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 37-38; 98pp; English
                                                                                                                                                                                                                                                           P-PSDB; AAY67206, AAY67214, AAY67215.
                                                                                                                                                                   BIOSCIENCES INC
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Matches 1477; Conservative
                                                                     98US-0087080.
98US-0141908.
98US-0100880.
99US-0119139.
                                     99WO-US11814
                                                                                                                                                                                                       Betlach MC,
                                                                                                                                                                                                                                           WPI; 2000-072618/06.
                                                                                                                                                                       (KOSA-) KOSAN
                                                                                           28-AUG-1998;
22-SEP-1998;
08-FEB-1999;
                                     27-MAY-1999;
02-DEC-1999
                                                                           28-MAY-1998
                                                                                                                                                                                                           Ashley G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of ORF14 which encodes dNDP-glucose 4,6-dehydratase.
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a C12-hydroxyalse (plcK), desosamine biosynthesis and desosaminyl transferase enzymes (useful for conversion of ketolides to antibiotics), and the beta-glucosidase enzyme (involved in picromycin biosynthesis). These compounds are also useful for increasing the antibiotic activity of a compound relative to the unhydroxylated compound. The recombinant host calls are useful as genetic systems that allow rapid engineering of the narbonolide polyketide synthase. These would be valuable for creating novel ketolide analogs for pharmaceutical applications.
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                                                                                                                                                       Query Match 7.7%; Score 529; DB 21; Length 3292; Best Local Similarity 53.4%; Pred. No. 3.1e-57; Matches 1476; Conservative 0; Mismatches 1180; Indels 109
                                                                                                                             Sequence 3292 BP; 521 A; 1290 C; 1044 G; 436 T; 1 other;
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Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolyymer; antibiotic; chemotherapeutic; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.
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                   GGACGCCTCGCGCGGACCGTCCGCTGCTACCGGGAGACCGCGGCTGGTGGGAGCCGCT
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Comportains a desosanthe biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, plkromycin, nachomycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, plkromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful for synthesis of methymycin, plkromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) custiut propagnes. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholasterol-lowering agents or macrolides the proper control of antibiotics which are active against a variety of organisms, e.g., characterial active against a variety of organisms, e.g., characterial active against a variety of organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine blosynthetic gene cluster from Streptomyces venezuelae ATCC 15439.
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0; Mismatches 1181; Indels 109; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              gene clusters, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthesis of methymycin and pikromycin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 281-287; 438pp; English.
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                       Streptomyces venezuelae ATCC15439
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Best Local Similarity 53.38
Matches 1475; Conservative
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                                                                     WO200000620-A2
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                                                                                                                      06-JAN-2000
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CGCCGGCGCGCGCCCCACGCCCCGAGGCCCATCATGTCGCTGCCCCACATGACGGCG 4692 6970 GCGACCCCCGTGCCCGTGCGCGCGCGCGACCCCCCCCGCTGCTGCTC 6911 4632 4460 7091 CCCCATCGCCTTGACGGGCT-----GTCTGATGGTGGTCAGGGGAGGGTCGGTGAAG 4572 7211 gagacciaccicicidarcicccicidarcicrcacricidegiciacirciccicida 1151 4461 TICGGIGCGCGGCGGCGTTCCGCTCATCTCCTCCAGCAGTGCGTCCACGGCGACCTG 4520 4404 7271 4293 GCTCGCCGCGACATGACGTCGG------GCCGGACCGCAACCACGGCCCCGGCCGG 4344 4173 7391 CAICGGGGGGGGGCACCICGCIGCCCAACCIGGAGCICACGCACCGGTIGCICGCACIGIG 4113 GGCGCTCGCCCACCGCACCGCCTGGACGTCCGGGTGACCCTGTTCGAACAA 3873 3753 GAGCGACCCCTGCTTCCGACCTCGCCGTACGCGCGTCGAAGGCGGCCTCGGACCTCAT 3813 3693 7931 CCACITCGCGGCCGAGAGCCACGTGGACCGCTCCATCGCGGGCGCGTCCGTGTTCACCGA 7991 GAGGTGATCGTCCCCTCGCACGTACATCGCCAGCTGGCTCGCGGTGTCCGCCACCGGC 7150 CICGAAAGATICGAGGGGGAGTICGCGGGGGACGGAGACGGACACGCCGTCGGCGTG 4573 GCCATGACGGGGAAGTCGTCGAAGCCGACCACGGAGATGTCACCGGGAACCGTGAGACCC 7330 CAAGGCGACCCCGCAGCTGCCCGCCACCGCCGTGGAGGTGTCCGCGTGAGCAGCCGC 4405 CCCCGCGGGCGGCGGGGGGGGGCCCCCGGACCAC---CAGTTCCGGCATGAAGACGAA 4114 CGGCGGGGCCCGGGAGCGCATCGTCCACGTCGAGACCGCAAGGGGCCACGACCGGCGCTA 4234 GACCGCGGTGGCCGAACGCGCGAAGTGGTACGAGCGGCACGAGGACTGGTGGCGTCCCCT CACCAACGTGCTGGGCACCCAGGTCCTGGACGCCGCGCTCCGCCACGGTGTGCGCAC 1910 GACCAACGTGCAGGCACGCAGACGCTCCAGTGCGCCGTCGACGCG 7030 4521 7210 4294 4174 7450 7390 1690 4054 3934 3754 7870 3814 7810 8050 3634 ð 셤 δ g 셤 ð g ŏ g ò ŏ g ö g δ g a õ g å g à a δ g δ g δý g ŏ ద õ

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/note= "No termination codon given in the specification"
/transl_except= (pos:8270..8275, aa:Yal)
/transl_except= (pos:8273..8275, aa:Thr)
/transl_except= (pos:8276..8278, aa:Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.
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/note= "No initiation codon given in the specification"
806..2014
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    GTGCAGCCCAGGTCGATCAGCGCGGACGCGG-CGGCCTGGCCCCCCCCCAGGGAGAACAG 4751
                             6910 GAGAAGGCGATCACCCCGCGACCCGGGCGCTCCTCCCCTACCGGCACCCC 6851
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trans1_except= (pos:6837..6841, aa:Gln)
492..8205
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complement (7942..8205)
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                                                                                                                       6850 GCCGACATGGACGCCCTCCGCGGACCGGCACGGCCTGCACATCGTCGAGGAC
                                                                                         4752 GAGTGCTGCACGAGCTCCTCGGACTCCCGCGCCGACACTCCCAGGTGCTCCCGCACGCC
                                                                                                                                                                                      GGCCCGGAACCCCTCGATCTTCCGCTGCACCGGCACGAAGCGGCGGGCCCGACGCGAG
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                                                                                                                                                                                                                                                                                  GCCGACGCGCTCGTGCCCCAGGTCCGCCAGGCCCAGGCGCCATCGCGGCCCCG
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    S. venezuelae desosamine biosynthetic gene cluster pikB.

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The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster of fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pixcomycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosanine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins and/or macrolide biosynthetic gene clusters are useful for synthesis of methymych, pixromycin, neomethymycin and care useful for synthesis of methymych, pixromycin, neomethymycin and care useful for synthesis of methymych, pixromycin, neomethymycin and care useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., antibiotics which are active against a variety of organisms, or as crop protecria, including multi-drug resistant pneumococci and other ceptratory pathogens, as well as viral parasitic pathogens, or as crop protecrial agents (e.g., fungicides or insecticides) via expression of protecrial agents in figure 32.
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                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY77204, AAY77205, AAY77206, AAY77207, AAY77207, AAY77209, AAX77210, AAX77211, AAY77212, AAX80999.
                                                                                                                                                                                                                                  /product- "PikB gene cluster protein #9 (AAY77210)"
complement (13706..15043)
/product= "PikB gene cluster protein #7 (AAY80999)"
complement (11271..12149)
                                                                                                                   /product= "PikB gene cluster protein #8 (AAY7209)'
complement (12342..13799)
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Matches 1475; Conservative
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8918 CGCAGGCTCACCGACTGGTGATCGGCGACCACAGGAAGGTGTATCTCACCCCATGACCAC 3339 3400 GTCGCCCGGGGCCCCCG-----GCGGCGTCGCGGTGACCGTCCTCGACAACTCACTA 3453 9129 6906 3159 TCGAGGACAGGGCCATCGAGTACTCCGTCCTGCTGCGGGGGCGCCCAGGTCGAGGGGGGGT 3219 2862 2919 2979 9269 3039 9242 3099 9182 2802 9389 2742 GACCATCCTCGTCACCGGCGGACGGCTTCATTCGCTCCGCCTACGTCCGCCGGCTCCT GTGCCGTCGTCAGCACTCCAGTGTCGGCCCGTACACCTÇCATCGGGGAGGACTGCCGGG CCCGCATCGAAGGCTCCCTCATCGGCCGCGGCGCCGTCGTCGGCCCGGCCCCCCTCTCC CCGACAGTGCGACCCACACGCGACCGCCCACCGACACGACACGCGACCC------3040 TGGCCGAAGGCGCGATCGTGCGGGGGTCACGTGGTGGGCCCCGGTGGTGATCGGCGCGG GCCTTGAGGAGATCGCCTTCCGCATGGGCTTCATCGACGCCGAGGCCTGTCACGGCCTGT 9181 GAGAAGGCCTCTCCCGCACCGAGTACGCCAGCTA-----TCTGATGGAGATCGCCGGC 2863 TGCAGTGGATGATCGACCGGGGCCTACGGGCCGA--GACCACCACCGGCCT ACGGGTCTACCTGGAGGGGGGGGGGGCGAACTCGTCAACCTGGGCGGGGGTTCGCCT **rgarggccgcatcgagggaaggtcgacgcacacacactggtcggccgggtccgg** GGGACAGCATCGCGCGCCTCGACGGCTGCTCTTCGGCTACCCGGTCAAGGACCCCG CCGACGICCCGCGCAGCICGCICGCGCTCAICGGCGTGTACGCCTICAGCCCGGCCGICC 9688 CCTGCGCCCTGATCCTGGGCGAACATCTTCCACGGGCCCGGCCTCTACACGCTCTGC GCCAATCGGCCGCCGATCCCGCGGCGGCCGGCTGCTGCTCACCCCGGTCGCGGACCCGT ACTICCTGCTGTACCTGGGGGACAACTACCTGCCC---CAGGGCGTCACCGACTTCGCCC AGAGCCCGCAGGAATCGCGGACGCACTCTCTCGTCGGACGCACACATCGGCGACGACACA CCCGCCCCCTCGGTCTCGCGGCGCGCGCTCCCCGCGGCTTCCTGGGCGACGACG TCGCCGCGCGGGTGTCCGGGAGGCCGGCGTCGTCGTGGGCGCGTACGGCCGGGAGATCC 3340 8977 3160 3220 8906 3280 9018 3100 9388 9328 2980 9268 9241 2920 2623 9628 2743 9208 8086 2506 9748 9868 2449 9928 2389 쉽 8 8 g õ ò oy oy oy ò g S a o o o o 9 9 9 g & 90 OX OD OX ò

7898 GAGACCGACGCCGCGATCGCCCCGCGTCCTCGGCGGCGCTACCTCCTCGGACCCGAA 7838 TTCGGTGCGCGCGCGCGTTCCGCTCATCTCCTCCAGCAGTGCGTCCACGGCGACCTG 4520 8018 4404 8138 4233 8078 4344 4053 GCCGAGACCCCCCCGCCTTCCTCGACCTCAAGGCCGCCTACGAGGAGCTCCGCGC GCTCGCCGCGACATGACGTCGG-------GCCGGACCGCAACCACCGGCCCCGGCCGG CACACCGCCGCCGGCGGGCCGGCCGGTCAGCGTCGGTGAGCCGGGGGCCGGCGG CGGCGCGGGCCCGGAGCGCATCGTCCACGAACCGCAAGGGCACGACGGCGCTA GACCGCCTGGCCGACACCGCGAAGTGGTACGAGCGGCACGAGGACTGGTGGCGTCCCCT CATCGGGGGGGGGCACCTCGCTGCCCAACCTGGAGCTCACGCACCGGTTGCTCGCACTGTG CGGCGCCACCGTTCCCCTTACGGCGACGGCGCACGTGCCGCGACTGGACGTCGA CACCAACGTGCTGGCAACCCAGGTCTGCACGCCGCGCTCCGCCACGGTGTGCGCAC GCACTTCGCGGCCGAGTCGCACGTCGACCGCTCCATCACCGACAGCGGTGCCTTCACCCG cecesesesearaceceargaseceseargasearceresacasecerasera CGCCGGCAGCTCGCCCGCCTGCACGCGGTGCGTGACCATCCCGGCCTCACCTTCGTCCA 4345 7897 4461 8137 4234 8077 4294 8017 7957 4174 8197 8377 3994 8317 4054 8257 4114 8497 3934 3814 3694 3754 8557 8617 3574 8737 3634 8677 8857 3514 8797 8917 3454 a ò ö g οy g δ <u>_</u> 6 g ŏ g ò 8 ò g g ŏ δ ò 셤 à g g ŏ 셤 ò g ò q ò g ò g ò g à

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 Glycosylated polyketide; modified recombinant bacterial host cell; mRBHC; macrolide; anthracycline; angucycline; avermectin; milbemycln; tetracycline; polyene; polyether; ansamycin; isochromanequinone; sugar; desosamine; des; gene; ds.
7718
                                                  4632
                                                                                 4633 GCCGGCGCGCGCCCGCACGCCCGAGGCCCATCATGTCGCTGCCGCACATGACGGCG 4692
                                                                                           GGACCCCCGTCGAGCCGCACCACCACCCACCCTGGACCCCTCGTC 7598
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                 4521 CCCCATCGCCTTGACGGGCT-----GTCTGATGGTGGTCAGGGGAGGGTCGGTCAAG 4572
                                                                                                                   4751
                                                                                                                                                                                                                                                              7360 GTCGTCACCGGCGACCCCCGAGCTCGCCGAACGCTCCGGATGCTCCGCAACTACGGCTCG 7301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Streptomyces venezuelae Des VIII protein"
/transl_except= (pos:806..808, aa:Met)
/note= "CDS does not include start codon"
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encoded protein #1"
806..2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product= "Streptomyces venezuelae Des VI protein"
                                                                                                                                                           GTGGCCGCGTTCAGCTTCTACCCGGGCAAGAACCTCGGCTGCTTCGGCGACGGCGGCGCC
                                 AACAGCGGGATGGACGCCCTCCAGCTCGCCCTCCGGGCCTCGGCATCGGACCCGGGGAC
                                                 GCCATGAGCGGCGAGTCGTCGAAGCCGACCACCGAGATGTCACCGGGAACCGTGAGACCC
                                                                 GAGGTGATCGTCCCCTCGCACACGTACATCGCCAGCTGGCTCGCGGTGTCCGCCACCGGC
                                                                                                                  GTGCAGCCCAGGTCGATCAGCGCGGACGCGG-CGGCCTGGCCCCCCCTCCAGGGAGAACAG
                                                                                                                                                  4752 CGAGTGCTGCACGAGCTCCTCGGACTCCCGCGCCGACACTCCCAGGTGCTCCCGCACGCC
                                                                                                                                                                                  Streptomyces venezuelae desosamine gene cluster.
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The invention provides a method to alter the sugar structure diversity for a particular metabolite via the recruitment and collaborative action of sugar genes from a variety of sugar biosynthetic pathways to yield a metabolite comprising a non-natural sugar, e.g., a novel gyvosylated polyketide. The invention also relates to a modified recombinant bacterial host cell (mRBHC) in which the expression and activity of nucleic acids encoding sugar biosynthetic enzymes has been altered. The mRBHCs may be cultured to produce the modified sugar products, tetracycline, polyene, polyene, polyether, ansamycin or isochromaneguinone. The present sequence is Streptomyces venezuelae sugar (desosamine) biosynthetic gene cluster.
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AAE24234, AAE24235, AAE24236, AAE24237, AAE24347.
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/note= "CDS does not include start codon"
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/transl_except= (pos:7969..7967, aa:Met)
/note= "CDS does not include start codon"
                                                                                                                                                                   venezuelae Des R protein"
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/transl_except= (pos:12881..12883, aa.Met)
/note= "CDS does not include start codon"
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                                                                                                                                                                                                 /transl_except= (pos:4312..4314, aa:Met)
/note= "CDS does not include start codon"
/transl_except= (pos:3532..3534, aa:Met)
/note= "CDS does not include start codon
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P-PSDB; AAE24228, AA
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                                                                        4461 TTCGGTGCGCGCGCGCGTTCCGCTCATCTCCTCCAGCAGTGCGTCCACGGCGACCTG
                                                                                                                          AACAGCGGGATGGACCCCTCCAGCTCGCCCTCCGCGGCCTCGGCACCCGGGGAC
                                                                                                                                              4573 GCCATGAGCGGCGAGTCGTCGAAGCCGACCACCGAGATGTCACCGGGAACCGTGAGACCC
                                                                                                                                                            GAGGTGATCGTCCCCTCGCACGTACATCGCCAGCTGGCTCGCGTGTCCGCCACCGGC
                                                                                                                                                                                   CGCCGGCGCGCCCCCCCCCGACGCCCATCATGTCGCTGGCGCACATGACGGCG
                                                                                                                                                                                                                                                           CGAGTGCTGCACGAGCTCCTCGGACTCCCGCGCCGACACTCCCAGGTGCTCCCGCACGCC
                                                                                                                                                                                                                                                                                               4872 GCCGACGCGCTCGTGCCCCAGCTCCGCCAGGTGCGCCACGGCCAGGCGCATCGCGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                 acbE gene; acbF gene; acbA gene; acbB gene; acbC gene; acbD gene acbE gene; acbF gene; enzyme; alpha-amylase inhibitor; treatment; diabetes; ss.
                                   4405 CCCCGCGGCCGGCGGCGGTGGACCCCCGGACCAC----CAGTTCCGGCATGAAGACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S. glaucescens acbD DNA fragment.
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                                                                                                                                                                                  This sequence encodes a fragment of the Streptomyces glaucescens GLA.O acbD gene which has been generated via PCR. The acbD gene is involved in the acarbose biosynthesis pathway. This gene and other acarbose biosynthesis genes such as those represented in AAT76903 are useful for producing acarbose, which is an alpha -amylase inhibitor useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3651
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                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 522.6; DB 19; Length 546; Similarity 97.4%; Pred. No. 2.5e-56; Conservative 0; Mismatches 14; Indels 0;
                                                 int DNA molecule comprising genes for biosynthesis of - an alpha-amylase inhibitor useful in treatment of
                                                                                                                                                                                                                                                                                                                                                       Sequence 546 BP; 69 A; 235 C; 168 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA039093 standard; DNA; 2634 BP.
                                                                                                                                          Example 2; Page 7; 35pp; German.
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                                                                                                                                                                                                                                                                                                             treatment of diabetes.
WPI; 1998-033827/04
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Best Local Simi
Matches 531;
                                                 Recombinant
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The sequence is that of a 2634 BamHI fragment from Streptomyces nodosus which comprises the complete snoT sequence (encoding amphotheronolide B-dTDP-D- mycosaminyl transferase), the snoD sequence (encoding dTDP-D-glucose synthase) and the partial snoM sequence (encoding dTDP-D-glucose synthase) and the partial snoM isolated genes can be used for, the microbial synthesis of hybrid and glycosylated naturalk products in Actinomyces; increasing the secondary metabolite yield in Actinomyces; the isolation of enzymes in biosynthesis and their use in enzymatic synthesis; the glycosylation of cpas, by biotransformation in Actinomyces; the identification of structurally and functionally novel genes; and the screening of producers of secondary metabolites.
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                           snoT; snoD; snoM; microbial synthesis; actinomyces; hybrid;
glycosylated; natural products; prods.; sequencing; gene;
polymerase chain reaction; secondary metabolite biosynthesis; ss.
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Pred. No. 2.4e-53;
0; Mismatches 364; Indels
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    Streptomyces nodosus 2634bp BamHI fragment.
                                                                                                                                                 /*tag= a
/note= "snoM C-terminal"
416..1534
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/note= "snoT sequence"
1561.2628
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/note= "snoD sequence"
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P-PSDB; AAR34012, AAR38296, AAR38297.
                                                                                                                   Location/Qualifiers
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Stockmann M, Taleghani KM;
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Matches 716; Conservation
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                                                                                         Streptomyces nodosus DSM40109.
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                                                                                                                                                                                                                                                                                                The present sequence represents the nogalamycin biosynthesis gene cluster isolated from Streptomyces nogalater. Nogalamycin is an anthracycline antibiotic, so the nogalamycin biosynthetic pathway is also known as the anthracycline biosynthetic pathway. DNA fragments, plasmids and process from the present invention are useful for obtaining novel hybrid antibiotics, such as anthracyclines (antitumour antibiotics)
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                                                                                                                                                                                     P-PSDB; AAY91055, AAY91056, AAY91057, AAY91058, AAY91059, AAY91060,
AAY91061, AAY91062, AAY91063, AAY91064, AAY91065, AAY91066, AAY91067,
AAY91068, AAY91069, AAY91070, AAY91071.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8350 TGGGTCGAGGGGCGCACTCCGCCCCACGGCACCCGACGGATGGAGGGAACCCATGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8170 TACGCGTCACCGTCCTCGACAAACTGACGCGGGCAACCTCACGAACCTGGACGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 16020;
                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                 Isolated and purified DNA fragment for obtaining novel hybrid antibiotics comprises the gene cluster for the anthracycline biosynthetic pathway of the bacterium Streptomyces nogalater .
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16020 BP; 2295 A; 6011 C; 5425 G; 2189 T; 100 other;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 486.8; DB 21; Length
Pred. No. 3.8e-52;
0; Mismatches 532; Indels
  ds,
 antibiotic; anthracyclinone;
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                                                                                                                                                        Hakala
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                                                                                                                                                                                                                                                                             Claim 2; Page 32-40; 59pp; English
                                                                                                                                                       Palmu
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.1%;
Best Local Similarity 61.7%;
Matches 910; Conservative
                                                                                                           98FI-0002295
                                                                                      99WO-FI00870
                                                                                                                                                       'n
 antibiotic; antitumour
                     Streptomyces nogalater
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                                                                                                                                 (GALI-) GALILAEUS OY
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                                                                                                          4083 TGGAGCTCACGCACCGGTTGCTCGCACTGTGCGGCGCGGGGCCCGGAGCGCATCGTCCACG
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TCGACGCCGCCGCCCACGGTGTGCGCACCTTCGTGCACGTCTCCACCGACGAGGTGT
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                                           TGGACGCCGCCGCCCACGCCGTGGAGCCCTTCGTCCTGGTGTCCACGGACGAGGTCT
                                                                                      ACGGCTCCCTCCCGCACGGGCCGCCGCGGAGAGCGACCCCCTGCTTCCGACCTCGCCGT
                                                                                                                                                                          TGGACGTCCGGGTGACCCGCTGTTCGAACAACTTCGGCCCCCCACCAGCATCCCGAGAAGC
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DNA;

standard;

AAF88341

RESULT 14
AAF88341
ID AAF88

3602

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                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel method nucleic acid (I) and its encoded composition of polypeptide (II) containing at least one region that encodes an enzymatic polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (I) to denerate a library of polyketide synthases; (II) for (II); (II) to generate a library of polyketide synthases; (III) for consamine or trimethylrhamnose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding consames, which are used for production of (II), their precursors or derivatives, including production of transgenic plants that express of derivatives, including production of transgenic plants that express (C and thus have increased resistance to insects. (I) are also useful as macrolides with insecticidal, but not antibacterial, activity, and can macrolides with insecticidal, but not antibacterial, activity, and can calso be used to raise specific antibodies, useful for identifying consponence consumptions of also be used to raise specific antibodies, useful for identifying consponence consumptions and agene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of consumptions of all produce new derivatives of consumptions of a spinosa genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCAGCCTCGCCCGCTGCACGCGGTGCCTGACCATCCCGGCCTCACCTTCGTCCAGGGC 3517
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                                                                      Forosamine; trimethylrhamnose; polyketide synthase; blosynthesis; spinosyn; polyketide aglycone; transgenic plant; insect resistance; macrolide; insecticidal; dNTP-glucose-4,6-dehydratase; ds.
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 6.8%; Score 465.8; DB 22; Length 990; al Similarity 68.5%; Pred. No. 2.38-49; 660; Conservative 0; Mismatches 297; Indels 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 990 BP; 169 A; 338 C; 333 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                               Salas JA;
                                             S. spinosa DNA fragment encoding ORF23, SEQ ID 52.
                                                                                                                                                                                                                                                                                               Froede R, 'Velten R,
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7a; Page 336-337; 354pp; German.
                                                                                                                                                                                                                  99DE-1057268.
                                                                                                                                                                                                                                            99DE-1040596
                        (first entry)
                                                                                                                                    Saccharopolyspora spinosa
                                                                                                                                                                                                                                                                                                  Eberz G, Moehrle V,
                                                                                                                                                                                                                                                                                                                           WPI; 2001-267102/28.
P-PSDB; AAB70970.
                                                                                                                                                                                                                                                                          (FARB ) BAYER AG.
                                                                                                                                                                DE19957268-A1
                                                                                                                                                                                                                                               27-AUG-1999;
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                                                                                                                                                                                         08-MAR-2001
                        28-AUG-2001
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Rhamnose synthesis; glucose; glucose thymidylate; glucose dehydratase; epimerase; ketoreductase; gtt; gdh; epi; kre; insecticide; arachnid; Spinosyn biosynthetic enzyme; insecticidal microlides; nematode; insect; polyketide; ss.
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                                                                                                                                                                                                                                                                                                                                                               Saccharopolyspora spinosa DNA fragment containing Rhamnose genes.
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                                                                                                                                                 GACCCCCTGCTTCCGACCTCGCCGTACGCGCGTCGAAGGCGGCCTCGGACCTCATGGCG
                                                                                                                                                              CTCGCCCACCACCGCACCCACGGCCTGGACGTCCGGGTGACCCGCTGTTCGAACAACTTC
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TTCGCGGCCGAGTCGCACGTCGACCGCTCCATCACCGACAGCGGTGCCTTCACCCGCACC
             AACGTGCTGGGCACCCAGGTCCTGCTCGACGCCGCGCTCCGCCACGGTGTGCGCACCTTC
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88..1077
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AAZ21502
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This sequence is a DNA fragment of Saccharopolyspora spinosa, containing two genes involved in Rhamnose production. There are four enzymes involved in the production of rhamnose from glucose. The first is a glucose thymidylate transferase (gqt:AAY39322), the second is glucose to glucose thymidylate transferase (gqt:AAY39322), the second is glucose a glucose thymidylate transferase (gqt:AAY39322), the second is glucose. The first is a nepimerase (epi:AAY39323) and the fourth a ketoreductase (kre:AAY39322), kre and gdh genes are found in this sequence. These four enzymes are used during the biosynthesis of spinosyns are insecticidal microlides which are useful for the control of arachnids, nematodes and insects. Blosynthesis of spinosyns occurs via stepwise condensation and modification of carboxylic acid precursors generating a linear polykefide which is modified further. The DNA sequence AAZ1501 contains 24 genes and open reading frames involved in spinosyn biosynthesis, AAY39297-Y39319. The genes identified in S. Spinosyns as having a role in the production of spinosyns e.g. by mutagenesis, or interruption of steps in spinosyn biosynthesis. The modified spinosyns and any be a new insect control agent or serve as substrates for further chemical modification and the creation of new sequences from S. Spinosyns. The genes are also useful to isolate similar sequences from S. Spinosyns are also useful to isolate similar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New spinosyn biosynthetic genes from Saccharopolyspora spinosa, useful for production of insecticidal spinosyn compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3344 ATCCTCGTCACCGGCGGAGCGGGCTTCATTCGCTCCGCCTACGTCCGCCGGCTCCTGTCG 3403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 GGTGCGTACCCCGCATTCGCCGACGCCGACGTGGTCGTCGACAAGCTCACGCC 213
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68.5%; Pred. No. 2e-49;
Live 0; Mismatches 297; Indels 6;
                                                                                                                                                                                                                                                                                                                                                  Crawford KP, Madduri K, Merlo DJ; Waldron C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2310 BP; 356 A; 759 C; 853 G; 342 T; 0 other;
/product= gdh
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1165..1992
                                                                               /product= kre
/note= "Ketoreductase"
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P-PSDB; AAY39320, AAY39321.
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Treadway PJ, Turner JR,
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AACGIGCIGGCACCCAGGICCIGCICGACGCCGCGCICCGCCACGGIGIGCGCACCTIC 3697
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                                                                                                                                           CTCGCCCACCACCCACCCACGCCTGGACGTCCGGGTGACCCCGCTGTTCGAACAACTTC
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Search completed: May 28, 2003, 16:40:43 Job time : 2176 secs

274 GACATCTGCGACCGCGAACTGGTTGGCGGCCTGATGTCCGGCGTGGACGTGGTGCTGCAC 333

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3578 TTGGGGGCCGAGTCGCACGTCGACGCTCCATCACCGACAGCGGTGCCTTCACCCGCAC 3637

IOTEM MULLE JOHN EIHT

SP0582 KR 1024034A0

AG030611 BG809984

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AW064148 BGB52363 BH606535 BBG809816 AG032943 BG809816 AG030608 BGB52363 AG030608

OM nucleic

Run on:

Sequence:

Title:

Searched:

Database

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Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 458)

NIH-MG http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

ECO RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CLONA Library Preparation: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.
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AW501598 UI-HF-BPO
AW501020 UI-HF-BPO
AG171124 Pan trog1
AW501038 UI-HF-BPO
BM617808 170006871
                                                                                May 28, 2003, 15:56:20 ; Search time 5709 Seconds (without alignments) 19443.662 Million cell updates/sec
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         GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pan trogl BOHMX80TF

AL249930 AG060010 BH512739

Pan trogl Pan trogl Pan trogl

AG041123 AG039481 AG043477 AG043469

Pan trogl BJ037676

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                                                                                                        /note="Vector: pT/T3"-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (4.4-7.4kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Latima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
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Pred. No. 5.1e-11;
0; Mismatches 161; Indels 12;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                                                                     B cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               435 bp mRNA
UI-HF-BP0p-ajg-d-07-0-UI.rl NIH_MGC_51
IMAGE:3074340 5', mRNA sequence.
AW501598
/organism="Homo saplens"
/db_xref="taxon:9606"
/clone="Inha"NIH_MGC_51"
/clone_lib="NIH_MGC_51"
/tissue_type="lymph"
/cell_line="MGCB5"
/lab_host="DH10B (LTI)"
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AWS01020 436 bp mRNA linear EST 01-MAR-2000 UI-HF-BPOp-ais-d-10-0-UI.il NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072834 5', mRNA sequence.
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NIH-MCC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: M.C. Cone distribution information can ifound through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/lmage.html
Seq primer: M.3 Forward.
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Pred. No. 3.6e-10;
0; Mismatches 147; Indels 12;
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/cell_line="MGG85"
/lab_host="DH10B_[LII]"
                                                                                                                                               Location/Qualiflers
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AW501020.1 GI:7114157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.9%;
Best Local Similarity 61.1%;
Matches 250; Conservative
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Chases 1 to 1798)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan
(E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-50-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3911 CGCTTCCTGACCAGCCTCCTGTCCGGCGCCACCGTTCCCCTCTACGGCGACGGCGGCGAC 3970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
778 c 655 g 0 t 365 others
                                                                                                                            Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
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/organism="Pan troglodytes"
/db.xref="taxon:9598"
/clone="RP43-040F09.TJ"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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4; Conservative
         Pan troglodytes
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R.Site 2
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Matches 614;
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Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-040F09.TJ.
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                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llni.gov/bbrp/image/image.html
Seq primer: Mi3 Forward
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Pan troglodytes DNA, clone: RP43-040F09.TJ, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="germinal center B cells"/cell_line="MGC85"
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/db_xref="taxon:9606"
/clone="InAGE:3072834"
/clone=lib="NIH_MGC_51"
/tissue_type="lymph"
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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AG171124.1 GI:16700802
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Unpublished (1999)
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Best Local Similarity
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CCGGGCGCCGGCCCCCGCGGCGGCGGGGGGGGCCCCCGGACCACACAGTTCCGGCA
                                     TGAAGACGAATTCGGTGCGCGGCGGCGTTCCGCTCATCTCCTCCAGCAGTGCGTCCA
                                                                           CGGCGACCTGCCCCATCGCCTTGACGGGCTGTCTGATGGTGGTCAGGGGAGGGTCGGTGA
                                                                                             4691 CGGTGCAGCCCAGGTCGATCAGCGCGGACGCGGCG----GCCTGGCCCCCTCCAGGGAG
                  4571 AGGCCATGAGCGGCGAGTCGTCGAAGCCGACCACCGAGATGTCACCGGGAACCGTGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="Discrete" (III)"
//lab_host="Netching (III)"
//note="Vector: pr713-Pac; Site_1: NotI; Site_2: Eco RI;
//note="Vector: pr713-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(4.4-7.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
145 c 127 g 68 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        undublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llni.gov/pbrp/lmage/Image.html
Seq primer: Mi3 Forward.
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1580 GCGCCCGNCCGCNCGCGCGCCCCCGCGCGNCCNCGCGCGCGCGCGCCC 1638
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Bukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3072976"
/clone=!ib="NIH_MGC_51"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGG85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 125; DB 10; 1
Pred. No. 1.9e-09;
0; Mismatches 150;
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Best Local Similarity 60.4%;
Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                    Homo saplens
                                                                      GATGGC 5527
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TITLE
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BM617808 804 bp mRNA linear EST 25-FEB-2002 17000687160009 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 119600449709229 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitces (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)" 251 c 284 g 118 t
CATACCGCGCTTCCTGACCAGCCTCCTGTCCGGCGGCACCGTTCCCCTCTACGGCGACGG :3963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCAGCCGCTCCTGGATGAGCTCGCCGAGGACGCGCACGCGGTCGATCAGCCGGTCGCGC 1041
                                                                                            374
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                Score 117.8; DB 13; Length
Pred. No. 2.4e-08;
0; Mismatches 232; Indels
                                                                                                                                          3964 GCGGCACGTGCGCGACTGCTCGACGACCACGTCAGGGCCGTC
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/strain="RSP-ST (Reduced susc. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:7165"
/clone="19600449709229"
/clone=llb="A.Gam.ad.cDNA.blood1"
/dev_stage="Adult"
/lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: HoltRA@celera.com
Plate: NU01004AXP row: I
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                          African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                       BM617808.1 GI:18916030
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ilarity 52.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 804)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
Contact: Holt R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celera Genomics
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Submitted (02-A0G-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Prel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMBLIL14 1798 bp DNA linear GSS 09-JAN-2002 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-040F09.TJ.
man troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                      313 TCGATCACGCGCATGACCGCGTTCGCAATCGCGCACGACACCGGATTGCCACCGTACGTG 254
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                                                                             GAGGCGTACGCCCCGGGGTGGCCGCCTCCGGCCTGCGCAGCTTCCGCGCGTCCGGCCAGC
                                                                                                                    253 TTGAAGTAGCAGACGCCGGTGGCGGCAAAGCTTTCCGCAATCTCGGGCGTAGTGACGACC
                                                                                                                                                                                                                                                                                 /sex-"male"
/cell_type-"lymphocytes"
/clone_lib-"RPCI-43 Chimpanzee Male BAC Library"
1 778 c 655 g 0 t 365 others
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
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Direct Submission
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/db_xref="taxon:9598"
/clone="RP43-040F09.TJ"
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                   26;
Length 1798
                   Indels
                    0; Mismatches 900;
 Score 117.2; DB 1
Pred. No. 3.2e-08;
 1.7%;
al Similarity 41.5%;
656; Conservative
   Query Match
Best Local S:
Matches 656
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mgct002xdllf Magnaporthe grisea Appressorium Stage cDNA Magnaporthe grisea cDNA stage cDNA Magnaporthe BG809984 clone mgct002xdllf 5', mRNA sequence. BG809984.1 GI:14180964
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/strain="70-15" 148305"
/db_xref="taxon:148305"
/db_xref="taxon:148305"
/clone="inb="Magnaporthe grisea Appressorium Stage cDNA"
/clone=lib="Magnaporthe grisea Appressorium Stage cDNA"
/dev_stage="Germinated conidia on apprressorium-inductive
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Sordarlomycetes incertae sed1s; Magnaporthaceae; Magnaporthe.
CGCTGTCGTGGACGTTCCACAGGCGGCGGGCCTGGGTGGTGAGTGCCTCGACGACCTCCG
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Email: ralph_dean@ncsu.edu
Seq primer: T3 primer (AATTAACCCTCACTAAAGGG).
Location/Qualifiers
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Choi, W. and Dean, R.A.
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/note="Vector: pBlueScript SK(+) Vector; Site_1: EcoRI; Site_2: XhoI; The appressorium formation-specific cDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library contains over 55,000 clones with average insert size of 1.5 kbp."
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Pred. No. 2.7e-07;
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Chases 1 to 1341)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (12-805-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-tu, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:sla145-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the RsD process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib:PTB Chimpanzee Male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG030611 1341 bp DNA linear GSS 01-NOV-200
Pan troglodytes DNA, clone: PTB-003A20.F, genomic survey sequence.
AG030611
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                                                                                 GTCCGACCAGCTCGGCGCGCGCTGTCGCGCCGGCTGCTCGTAGCCCCAGCGCGTCAGTG
                                                               5057 CGGAGACGAAGATGATGCCGGACACCCCGCGGTCCACGAGCATCTCCGTGAGTTCGTCCT
                                                                                                                                   CGGTCGAGCCGCCCGGGGTCTGCGTGGCGAGCACGGGCGTGTAGCCCTGACGCGTGAGCG
                                                                                                                                                                                                    CCTGCCCCCATCACCTGGGCCAGTGCGGGGAAGAAGAGGGGTTGTCCAGTTCGGGGGGTGACCA
                               Taylor, T.D., Yada, T.,
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BAC Library clone:PTB-003A20.F.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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No. 5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
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/db_xref="taxon:9598"
/clone="PTB-003A20.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="lymphoblast"
/clone_lib="PTB Chimpanze
476 c 700 g 14
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Magnaporthe
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Seq primer: T3 primer (AATTAACCCTCACTAAAGGG).
Location/Qualifiers
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Pred. No. 6.6e-07;
0; Mismatches 698;
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Euteleostom1;

Craniata; Vertebrata; E Catarrhini; Hominidae;

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Metazoa;

ORGANISM

REFERENCE AUTHORS

TITLE

1 (bases 1 to 273)
60.5.-H., Park,J.-H., Lee,Y.J., Lee,H.G., Yoo,H.-S., Lee,I.-C.,
Park,J.-H., Kim,Y.-S. and Lee,C.-C.
Gene expression profile and identification of differentially
expressed transcripts during human intrathymic T-cell development
by CDNA sequencing analysis
Genomics 70 (1), 1-18 (2000)

of Bioscience and Biotechnology Daejon 305-333, Republic of Korea

Korea Research Institute Oun-dong 52, Yu Sung-Gu, Tel: 82-42-860-4473

Genome Center

Sung-Ho Goh

Contact: 20541704

JOURNAL MEDLINE COMMENT

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GAGTCGTCGAAGCCGACACCGAGATGTCACCGGGAACCGTGAGACCCCGCCGCGGCGCGC
                                                                                                                                         GCCCGCACGCCCCGAGGGCCATCATGTCGCTGGCGCACATGACGGCGGTGCAGG
                                                                                                                                                                            CCTCGATCTTCCGCTGCACCGGCACGAAGCGGGCGGGCCCGACGGCGAGGCCGACG-CGC
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                                                  ATCGCCTTGACGGCTGTCTGATGGTGGTCAGGGGAGGGTCGCTGAAGGCCATGAGCGGC
                                                                                                                                                                                                                                                     AGCTCCTCGGACTCCCGCGCCGACACTCCCAGGTGCTC - - CCGCACGCCGGGCCCGGAACC
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Length

DB 10;

1.6%; Score 108.2; DB 10; 62.3%; Pred. No. 6.2e-07; 1ve 0; Mismatches 103;

Conservative

Similarity

Best Local Sim Matches 170;

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Query Match

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BASE COUNT ORIGIN

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3809 CTCATGGCGCTCGCCCACCACCGCACCGCCTGGACGTCCGGGTGACCCGGTGTTCG 3868

AACAACTTCGGCCCCCACCAGCATCCCGAGAAGCTCATACCGCGCTTCCTGACCAGCCTC 3928 61 AACAACTACGGCCGGTTCCACTTCCCGGAAAAGCTGATTCCGCTGGTAATCCTCAACGCC 120

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121 3989 181

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CTGTCCGGCGCACCGTTCCCCTCTACGGCGACGGCGCACGTGCGCGACTGGCTGCAC 3988

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241

/cell_type="Thymus" /cell_type="Intrathymus" /cell_type="Intrathymuc T-cell" /dev_stage="Coll_type="Intrathymuc T-cell" /dev_stage="Coll_type="Coll_type="Intrathymuc Coll_type="Coll_type=

CDNA

CD4 intrathymic T-cell

.273
 /organism="Homo sapiens" /db_xref="taxon:9606"
 /clone_lib="KRIBB Human (

library

High quality sequence stop: 273 POLYA-No.

Location/Qualifiers

source

FEATURES

Email: gohsh@mail.kribb.re.kr

Fax: 82-42-860-4479

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EST 29-MAY-2001
Lambda 2ap II
                                                                                                                        Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                      1281 bp mRNA linear 1024034803.y2 C. reinhardtii CC-1690, normalized, Chlamydomonas reinhardtii cDNA, mRNA sequence. BG852363
                                                                                            GI:14233547
                                                                                           BG852363.1
                                                                                                             EST
                                             DEFINITION
                                                                                                                                          ORGANISM
RESULT 12
BG852363
LOCUS
                                                                            ACCESSION
                                                                                                           KEYWORDS
SOURCE
                                                                                           VERSION
                                  SPOSS. RIBB Human CD4 intrathymic T-cell cDNA library Homo sapiens AW064148
AW064148
BST.
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human.

RESULT 11
AW064148
LOCUS
DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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3625 CTTCACCCGCACCAACGTGCTGGGCACCCAGGTCCTGCTCGACGCCGCGCTCCGCCACGG
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XhoI; This library, constructed by John Davies and Jeffrey
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines colNas from cc-1690 cells grown to
mid-log phase in TaP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in the
light ambient levels of Co2 and HS medium bubbled with 5% CO2
mubient levels of Co2 and HS medium bubbled with 5% CO3.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The CDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRN (5%) and XNOI (3%) sites
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_llb="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGACATCGTGCACTTCGCGGCCGAGTCGCACGTCGACCGCTCCATCACCGACAGCGGTGC 3624
                            1 (bases 1 to 1281)
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydononas reinhardtil Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2
Unpublished (2000)
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 106.8; DB 12;
Pred. No. 1.1e-06;
0; Mismatches 678;
            Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: chauser@duke.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Contact: Charles Hauser
DCMB Box 91000
Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6%;
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Tel: 919 613 8159
Fax: 919 613 8177
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                                                             REFERENCE
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BH606535 15-DEC-2001
BOHAT59TR BOHA Brassica oleracea genomic clone BOHAT59, DNA
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Brassica oleracea
Brassica oleracea
Brayophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 828)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSS: BOHAT59TF
Contact: Chris Town
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                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                           Length 828;
                 Tel: 301-838-3525
Fax: 301-838-0208
Email: cdtownetigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq prime: TR
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                     Score 104.6; DB 17; Length
Pred. No. 2.4e-06;
0; Mismatches 329; Indels
            MD 20850,
                                                                                                           /organism="Brassica oleracea"
/strain="To1000H3"
/db_xref="taxon:3712"
            Rockville,
            Center Drive,
                                                                                                                                             /clone="BOHAT59"
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llarity 50.9%;
Conservative
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mgct001xk18f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe grisea cDNA Magnaporthe grisea Appressorium Stage cDNA Magnaporthe grisea cDNA clone mgct001xk18f 5', mRNA sequence.
BG809816.1 GI:14180796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBlueScript SK(+) Vector; Site_1: ECORI; Site_2: XhoI; The appressorium formation-specific cDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library contains over 55,000 clones with average insert size of 1.5 kbp."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:148305"
/db_xref="taxon:148305"
/clone="mgct001xk18f"
/clone_lib="Magnaporthe grisea Appressorium Stage cDNA"
/dev_stage="Germinated conidia on apprressorium-inductive surface"
                                                                                                                                               Magnaporthe grisea.
Magnaporthe grisea
Bukaryota, Fungi, Ascomycota, Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 1651)
Choi, W. and Dean, R. A.
Construction and sequence analysis of an appressorium stage cDNA library in the rice blast fungus, Magnaporthe grisea
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Pred. No. 2.5e-06;
); Mismatches 850; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ralph_dean@ncsu.edu
Seq primer: T3 primer (AATTAACCTCACTAAAGGG)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     grisea"
                                                                                                                                                                                                                                                                                                                                          Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695,
Tel: 919-513-0020
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/organism="Magnaporthe
/strain="70-15"
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                                                                                                                                                                                                                                                                                                                        Contact: Ralph A. Dean
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TITLE
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Taylor, T.D., Yada, T.,

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan

Fullyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library PTB

Unpublished

TITLE JOURNAL REFERENCE

AUTHORS

AUTHORS

REFERENCE

JOURNAL

TITLE

Upses 1 to 1542)

Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-Chou, Tsurumi-tu, Yokohama, Kanagawa 230-0045, Japan

(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:iB1-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of

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3499
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GCTGGTCGGCCGGGTCCGGGTGGCCGAAGGCGGGATCGTGCGGGGGTCACACGTGGTGGG 3079
                                              CCCGGTGGTGATCGGCGCGGGGTGCCGTCGTCAGCACTCCAGTGTCGGCCCGTACACCTC 3139
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Length 1542;

/ccl_type="lymphoblast" /clone_lib="PTB Chimpanzee Male BAC Library" 657 c 614 g 19 t 191 others

/organism="Pan troglodytes" /db_xref="taxon:9598" /clone="PTB-007N10.F"

/sex="male"

61

BASE COUNT ORIGIN

Location/Qualiflers : pKS145 : Saci : Saci

source

FEATURES

R.Site 1 R.Site 2 Vector

Sequencing: -21M13 clone tracking errors.

PRIMERS LIBRARY

COMMENT

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1147
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                                                                                                  19;
Query Match
1.5%; Score 104.2; DB 17; Length
Best Local Similarity 43.3%; Pred. No. 2.8e-06;
Matches 544; Conservative 0; Mismatches 694; Indels
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Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male MaC Library clone:PTB-007N10.F. Pan troglodytes Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AG032943 11near GSS 01-NOV-2001 Pan troglodytes DNA, clone: PTB-007N10.F, genomic survey sequence.

AG032943.1 GI:16559816

GSS.

KEYWORDS VERSION

ORGANISM

DEFINITION ACCESSION

RESULT 15 AG032943/c

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1564
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                                                                                                     1265 CGGTGAGGACCTCGTCGCGGACGAGCAGCACGCCGTCCCGGCAGGCGCCGCGGCGATCC 1324
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Search completed: May 28, 2003, 21:04:52 Job time : 5799 secs

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Appli

Perfect score:

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Scoring table:

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ISOLATION OF THE BIOSYNTHESIS GENES FOR PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS GLA.O AND THEIR USE
                                                                                                        Sequence 1, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 1, Appl
Sequence 3, Appl1
Sequence 5, Appl1
Sequence 5, Appl1
Sequence 19, Appl
Patent No. 5221737
Sequence 13, Appl
Sequence 2, Appl
Sequence 7, Appli
                                                                                                                                                                                                                                                                               Sequence 26,
Sequence 28,
                                                     Sequence 1,
Sequence 1,
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APPLICATION NUMBER: US/09/194,905 FILING DATE: 29-JuL-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                US-09-103-840A-2
US-08-804-227C-7
US-08-804-198-1
US-07-945-283-1
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US-09-105-537-1
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US-09-543-084A-28
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US-09-105-537-5
US-09-320-878-19
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US-08-843-659-1
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP97/02826
FILING DATE: 30-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19622783.6
FILING DATE: 07-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Granados, Patritida D.
REGISTRATION NUMBER: 33,683
REFERENCE, DOCKET NUMBER: 026083/0193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09194905
Patent No. 6306627
GENERAL INFORMATION:
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100.0%;
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(202) 672-5399
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TYPE: nucleic acid
STRANDEDNESS: single
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TITLE OF INVENTION: ISOI
TITLE OF INVENTION: GLA
TITLE OF INVENTION: GLA
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         13842
36778
38506
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CITY: Washington
STATE: D.C.
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Best Local Similarity
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1 CTGCAGGGTTCCCTGGTGCA.....TCGAGCCGATCCGGCTGCAG 6854
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Sequence 8,
Patent No. 52
Sequence 28,
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Sequence 12
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Sequence 1,
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/cgn2_6/ptodata/1/ina/5B_COWB.seq:*
/cgn2_6/ptodata/1/ina/6A_COWB.seq:*
/cgn2_6/ptodata/1/ina/6B_COWB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COWB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COWB.seq:*
              GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-320-878-22

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US-09-1194-905-3

US-08-681-953-31

US-09-036-987A-25

US-09-036-987A-25

US-09-036-987A-25

US-09-036-987-25

US-09-105-537-13

US-09-105-537-13

US-09-105-537-13

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US-09-105-537-13

US-09-105-537-13

US-09-105-537-13

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US-09-370-700-28
US-08-961-527-1
US-09-105-537-11
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Maximum Match 100%
Listing first 45 summaries
                                                                                  - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1 AGTTCC 1 AGTGCG 1 1 1 1 1 1 1 AGTGCG 1 GGGTCGC	CATGAAGACGAATTCGGTGCGGGGGGGGGGGTTCCGCTCA CACGGCGACCTGCCCATCGCCTTGACGGGCTGTCTGATGGT
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¥ _ ¥ ~ %	AGGCCGACGCG
ATCGC ACGAC ACGAC	9 9 4
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5 - 5 5 - 5 5 - 5	CUCTEARGEGETTGECCATCACCATGGGCCAGTGGGGGAAGAAGGGTTGTCC 5220
AGTTC AGTTC	NGTTCGGGGGTGACCAGTCCGACCAGCTCGGCGCGCGCTGTCGCCCGGCTGCTCGTAG 5280
CCCAGG	SGGGTCCAGTGCGGTCAGCGACCGAGTGCCGGTGGCCACACCGCGCGCA 5340
CCGT1	CGTTCAGCACCGGCTGACCGTGGCTTGCTGACGCCCGCCGGGCTGCGATGTCGGCG 5400
AGCCG AGCCG	CATGGTCATGGCAACGCACTCTACCTGTCGGGCGTCAGGGCGTGCCCACGCGC 5460

Oy Ob	5461	GCGGAACCGGCCGCACTCCGGGGCACGCCCGTCCGCCGCCCACGGACCACGCGCCCGAAA 5520
qq.	5521 5521	ATGCTTGCAGCAAATTGCCGCAACG
yo oy	5581 5581	CCTGGCAACCCGGGGCGCGCAGAAGCGGTTGGCGTGAGGCGTCCAGACCT 56.
Oy Db	5641	CAGGGAGTTCACAATGCGGGGTGGCATTGCGGCCACCG 570
O.Y	5701	CTGTGGCCATGACGCCATCGCCGTGTGGCGGGGCGACAACGGCGGAA 576
ço Qu	5761 5761	TACCGACGCGGCGCGCACCTCTCGGGGACCGTCACCTTCTGGGACACGTCA 5
oy Ob	5821 5821	SAGAAĞGCGACGTACCAGGCCCTCGCGGAGGCTTCGAGAAGGAGCACCCGA 588
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Qy Dp	5941 5941	GGGCAACTCCGGTGCCCCGGACGTGATGCGTACGGAGGTCGCCTGGGTCGCGG 6
Qy Db	6001	TICGCCAGCATCGGCTACCTCGCCCCGCTCGACGCACGCCCCCCCC
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Qy	6121 6121	TCTTCTACAACAAGGAACTGCTGACGAAGGCCGGTGTCG 618
9 Q	6181	TICCTCGCCGAGCTGAAGACGGCCGCCGAGATCACCGAGAAGACCG 624
ço da	6241.	GGGGACGACCCGTACTTGGTTCCTGCCCTACCTCTACG 630
Qy QD	6301	CTGGTCGACGAGAAGAACAAGACCGTCACGGTCGACGAGGCG 636
Qy Db	6361 (GCCTACCGCGTCATCAAGGACCTCGTGGACAGCAAGGCGGCCATCACCGACG 64
Qy	6421 (AACATGCAGAACGCCTTCAAGTCGGGCAAGG
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                                                                              ACCTGGGGGTCGCCCCCGTCCCGGCCGGCAGTGCCGGACAGGGCTCTCCCCCAGGGCGGGT
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Pred. No. 2.5e-68;
0; Mismatches 1180; Indels 109;
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Patent No. 6117659
GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MODANIEL, Robert
APPLICANT: TANG, LI
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
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CURRENT FILING DATE: 1999-05-27
EARLIER PAPPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-06-28
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER APPLICATION NUMBER:
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Best Local Similarity 53.4%;
Matches 1476; Conservative
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JENGTH: 3292
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2682 3039 3220 CCCGCATCGAGGCGTCCCTCATCGGCCGCGCGCGCGTCGTCGGCCCGGCCCCCGTCTCC 3279 -----cacaccegacctacagcegaccgaaggaag------acegcagt 1115 1236 CGCGGGCAACCGCGCCAACCTCGCCCCGGTGGACGCGGGACCCGCGACTGCGCTTCGTCCA 1295 2622 3159 3160 TCGAGGACAGCGCCATCGAGTACTCCGTCCTGCTGCGGGCGCCCCAGGTCGAGGGGGGGT 3219 1025 CCGACAGTGCGACCCACCGCGACCGCCACCGACAGTGCGACC----- 1074 1176 CGCCGGGGCGTACCCCGACGTGCCCGCATGAGGTGATCGTCCTCGTCGACACCCTCACCTA 1235 3040 TGGCCGAAGGCGCGATCGTGCGGGGTCACACGTGGTGGGCCCGGTGGTGATCGGCGCGG 3099 964 464 225 TCATGCTCGCGGTATTCGCGAGATTCAAATCATCTCGACCCCCCAGCACATCGAACTCT 284 345 AAGAGCCCGCAGGAATCGCGGACGACCTTCTCGTCGGAGCCGAGCACTCGGGGACGACAACGACGACAAA 645 TCGACATCGCCAAGAACATCCGCCCTCGCCGCGCGGCGGCGACCTGGAGATCACCGACGTCA 285 TCCAGTCGCTTCTCGGAAAGGCCACCTGGGAATAGAACTCGACTATGCGGTCCAGA 2506 ccceccicerreserresesacses are served contracted co 2566 ACTICCIGCIGIACCIGGGGACAACIACCIGCCC---CAGGGCGICACCCGACTICGCCC 2623 GCCAATCGGCCGCCGATCCCGCGGCGGCCCGGCTGCTGCTCACCCCGGTCGCGGACCCGT 585 CCGTCAAGCCGCGCTCCAACCTCGCCGTCACCGGCCTCTACCTCTACGACAACGACGTCG 3100 GTGCCGTCGTCAGCAACTCCAGTGTCGGCCCGTACACCTCCATCGGGGAGGACTGCCGGG 912 GAGAAGGCCTCTCCCGCACCGAGTACGGCAGCTA----TCTGATGGAGATCGCCGGC 3280 CGCAGGCTCACCGACTGGTGATCGGCGACCACAGGAGGTGTATCTCACCCCATGACCAC 3400 GTCGCCCGGGGCCCCCG-----GCGGCGTCGCGGTGACCGTCCTCGACAAACTCACCTA 3454 CGCCGGCAGCCTCGCCCGCCTGCACGCGTGCGTGACCATCCCGGCCTCACCTTCGTCCA 465 GGGACAGCATCGCGCGCCTCGACGGCTGCGTGTTCGGCTACCCGGTCAAGGACCCCG 1683 CCGCCTTCGGCGTCGCGGAGGTCGACGCGGACGGGAACGTGCTGCGCTTGGAGGAAAC 2863 TGCAGTGGATGGACCGGGGCCTGCGCGTACGGGCCGA---GACCACCACCGGCCCT 705 ACCGCGTCTACCTGGAGCGGGGCCGGAACTCGTCAACCTGGGCCGCGCGCTTCGCCT 765 GGCTGGACACCGGCACCCACGACTCGCTCCTGCGGCCGCCCCAGTACGTCCAGGTCCTGG 2980 TGGAGGCCGCATCGAGGGGAAGGTCGACGCGCACAGCACGCTGGTCGGCCGGGTCCGGG 852 GCCTTGAGGAGATCGCCTTCCGCATGGGCTTCATCGACGCCGAGGCCTGTCACGGCCTGG 3340 GACCATCCTCGTCACCGGCGGAGCGGGCTTCATTCGCTCCGCCTACGTCCGCCGGCTCCT 405 CCTGCGCCCTGATCCTGGGCGACATCTTCCACGGCCCGGCCTCTACACGCTCCTGC 2743 CCGACGTCCCGCGCAGCTCGCTCGCGTCATCGGCGTGTACGCCTTCAGCCCGGCCGTCC

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3514 GGGCGACGTGTGCGACCACCGCGCCGCCGCGCGCGCGCACGACGACGACGA	94 CTTCGTGCACGTCTCCACCACGACGTGTACGGCTCCCTCC	3874 CTTCGGCCCCACCAGCAGCAGAAGCTCATACCGGCGTTCCTGACCAGCCTCCTGTC 3933 1656 CTACGGGCCGTACCAGCACCCCGAGAAGCTCATCCCCCTCTTCGTGACCACCTCCTCGA 1715 3934 GGGCGCACCGTTCCCCTCTACGGCGACGGCGGCACGTGCGGCTGCACGTCGA 3933 11111 1 1 1 1 1 1 1 1	CATCGGGGGGGGGGGGGGCTGGAGCTGGAGCTGCGGGGTGGTGGTGGTGGTGGTGGTGGGGGGGG
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                                       2376 GAGGTGATCGTCCCCTCGCACACGTACATCGCCAGCTGGCTCGCGGTGTCCGCCACCGGC 2435
                                                                              4633 CGCCGGCGCGCGCGCCCCACGGCGCCCAACATGTCGTCGCTGGCGCACATGACGGCG 4692
                                                                                                               2436 gegacedecedrecegregacedeacadaacadeceacecerecacegregacegregae 2495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09105537A

Patent No. 6265202

GENERAL INFORMATION:
APPLICANT: Liu, H.
APPLICANT: ALO, Y.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION UNDBER: US/09/105,537A

CURRENT FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3

LENGTH: 13613
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Best Local Simi
Matches 1475;
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CCGCCCGCTCGGTCTCGCGCACGCGGTGCGCATCGCCGCGGCTTCCTGGGCGACGACG 2565	ACTICTGCTGTGTGCGGGGGGACAACTACCTGCCCCAGGGCGTCACCGACTTCGCC 2622 	GCCAATCGGCCGCCGATCCCGCGGCGGCGCTGCTCACCCCGGTCGCGGACCCGT 2682 	CCGCCTTCGCCGTCGCGGACGTCGACGGGAACGTGCTGCTGCTGGAGAGAAAC 2742 	CCGACGTCCCGCGCAGCTCGCTCATCGGCGTGTACGCCTTCAGCCCGGCCGTCC 2802 	ACCAGGGGGTACGGGCCATCACCCCTCCGCCGGGGGGGGG	TGCAGTGGATCGACCGGGGCCTGCGCGTACGGGCCGAGACCACCACCGGCCCT 2919	GGCGCGACACCGGCAGCGCGGAGGACATGCTGGAGGTCAACCGTCCAGGACGGAC	TGGAGGCCCCATCGAGGGAAGGTCGACGCCACACCACGCTGGTCGGCCGGGTCCGGG 3039 	TGGCCGAAGGCGCGTCGTGGGGGGTCACACGTGGTGGGCCCGGTGGTGGTCGGCGGG 3099 GCCTTGAGGAGATCGCCTTCCGCATGGGCTTCATCGACGCCGAGGCCTGTCACGGCCTGG 9182	GTGCCGTCGTCAGCAACTCCAGTGTCGGCCCGTACACCTCCGGGGAGGACTGCCGGG 3159 	TCGAGGACACCCCATCGAGATACTCCGTCCTGCGCGCGCCCCCAGGTCGAGGGGGGT 3219	CCCGCATCGAGGCGTCCCTCATCGGCCGCGCGCCGTCGTCGGCCCGGCCCCCGTCTCC 3279	CGCAGGCTCACCGACTGGTGATCGCGACCAGCAAGGTGTATCTCACCCCTAGACCAC 3339 CACACCGACCTACAGCGACCGACGAAAGGAAGACGGCAGT 8978	GACCATCCTCGTCACCGGCGGGGCGTTCATTCGCTCCGCCTACGTCCGCCGGCTCCT 3399 	GTCGCCCGGGGCCCCCGGCGGCGTCGCGTCGTCCTCGACAAACTCACCTA 3453	CGCGGGCAGCCTGCCCGGCTGCGGTGCGTGCCGTCCGGCCTCCACCTTCGTCCA 3513	GGGCGACGTGTGCGACACCGCGCTCGTCGACACGCTGGCGCGCGC	
CCCGCCCGCTCGCTCCCGCACGCGGTGCG	ACTTCCTGCTGTACCTGGGGGACAACTACCT	GCCAATCGGCCGCCGATCCCGCGGCGGCGGCCG 	CCGCCTTCGCCGTCGCGGAGGTCGACGCGGA 	CCGACGTCCCGCGCACTCGCTCGCGCTCAT	ACGAGGGGGTACGGGCCATCACCCCTCCGC	TGCAGTGGATCGACCGGGGCCTGCGGT 	GGCGCGACACCGCGGAGGACATGCT 	TGGAGGCCGCATCGAGGGGAAGGTCGACGC 	TGGCCGAAGGCGCGATCGTGCGGGGGTCACA 	GTGCCGTCGTCAGCACTCCAGTGTCGGCCCGTACACCT 	TCGAGGACACGCCATCGAGTACTCCGTCCT 	CCCGCATCGAGGCGTCCCTCATCGGCCGCGG 	CGCAGGCTCACCGACTGGTGATCGGCGACCACCAGCAAGGTG	GACCATCCTCGTCACCGGCGGGGGGGTTC 	GTCGCCGGGGCCCCGGCGGCGTC 	CGCCGGCAGCTCGCCCGCCTGCACGCGGTG	GGGCGACGTGTGCGACACCGCGCTCGTCGAC 	
2506 C	2566 A	2623 G 9628 G	2683 C	2743 C 9508 C	2803 A	2863 T	2920 G 9328 G	2980 T	3040 T	3100 G	3160 T	3220 C 1 9068 C	3280 C	3340 G 1 8977 G	3400 G 8917 C	3454 C	3514 G 8797 C	
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oy e	3574 (GCACTTCGCGGCCGACGTCGCACGCTCCATCACCGACAGCGGTGCCTTCACCCG	3633
δ	634	CACCAACGIGCIGGCACCCAGGICCIGGACGCCGCGCTCCGCCACGGIGIGCGCAC	69
a č	3694	4 5	3753
QQ	8617		55
Οy	3754 (GACCACCCCTGCTTCCGACCTCGCCGTCGAAGGCGCCTCGGACCTCAT	3813
đ	8557	and can a contract co	
y g	3814 (GGCGCTCGCCCCCCCCCCCCCCCCCGCCTGGACGTCCGGGTGACCCGCTGTTCGAACAA	3873
Qy	874	TITCGGCCCCCACCAGCATCCCGAGAAGCTCATACCGCGCTTCCTGACCAGCCTCCTGTC	93
ති	8437		8378
oy G	3934 (CGCGGCACCGTTCCCTCTACGGCGACGGCGCACGCGCGACTGGCTGCACGCGCTCGA	3993
ò	994	:ACGTCAGGGCGTCGAACTCGTCGGCGTGTCGGGCC	05
g G	317		25
φ	4054	CATCGGGGGGGGGCGCACCTGCCCAACCTGGAGCTCACGCACCGGTTGCTCGCACTGTG	4113
đ	8257	ITTELLITIES DE LE LE LITTELLE DE LE	8198
O _Y	114	CGGCGCGGGGCCCGGAGCGCATCGTCCACGAGCAACCGCAGGGCCACGGCGCTA	17
අු	97	GGCGCCGACTGGTCCTCGGTCCGGAAGGTCGCCGACGGCAAGGGCCACGACCTGCGCTA	m
δō	74	CGCGGTCGACCACACAAGATCACCGCGGAACTCGGTTACCGGCCGCGCGCG	23
Q O	8137 (CTCCCTCGACGGCGGCGAGATCGAGCGCGAGCTCGGCTACCGCCCGC	8078
y g	4234 (GACCGCGCTGGCCGACCGCGAAGTGGTACGAGGCGGCACGAGGACTGGTGGCGTCCCTT	4293
δ		GCTCGCCGCGACATGACGTCGGGCCGGACCGCAACCACCGGCCCCGGCGG	34
qq	8017		95
ΟŊ	4345 (PACACCGCCGCCGGCGGGTGGCCGGTCAGCGTGAGCCGGGCCGGCC	4404
qq	7957 (GCCGAGACCCCCCCGCGTCCCCTTCCTCGACGCCGCCTACGAGGAGGAGCTCCGCGCG	7898
ογ	4405	CCCGCGGGCGGGGGGGGGGGGGGCCCCGGACCACAGTTCCGGCATGAAGACGAA	4460
q	16	GAGACCGACGCGCGCGCCCCCCCCCTCGACTCGGGGCGCTCTCCTCGGACCCGAA	7838
ΟŊ	4461	TTCGGTGCGCGCGCGCGTTCCGCTCATCTCCAGCAGTGCGTCCACGGCGACCTG	4520
qq	7837 (-ğ	7778
δλ	4521 (CCCCATCGCCTTGACGGCTGTCTGATGGTGGTCAGGGGAGGTCGGTGAAG	4572
qq	1777	acagogggarggacgccotocagorocgccotocgggcotogggarcggggc	7718
ογ	4573 (GCCATGAGCGGCGAGTCGTCGAAGCCGACCACCGAGATGTCACCGGGAACCGTGAGACCC	4632
ପ୍ର	7717 (GAGGIGATCGTCCCTCGCACACGTACATCGCCAGCTGGCTCGCGGTGTCCGCCACCGGC	7658
οy	4633 (CGCCGGCGCGCCCCCACGCCCCGAGGGCCCATCATGTCGCTGGCGCACATGACGGCG	4692

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Secondary-Metabolite Biosynthesis Genes From Actinomycetes, Method of Isolating Them, and Their
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CCIGCACGCGGIGCGIGACCAICCCGGCCICACCIICGICCAGGGCGACGIGIGCGACAC 3531
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                                                                                  Length 546;
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                                                                           Score 522.6; DB 4;
Pred. No. 2.1e-67;
0; Mismatches 14;
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APPLICANT: Stockmann, Michael
APPLICANT: Taleghan1, Kamplz Mansour1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/08196218 Patent No. 5614619 GENERAL INFORMATION:
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   DNA (genomic)
                                                                                        7.68;
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STREET: 1300 I Street,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Secrific OF INVENTION: From TITLE OF INVENTION: Use NUMBER OF SEQUENCES: 34 CORRESPONDENCE ADDRESS:
                                                                                        Query Match 7.69
Best Local Similarity 97.49
Matches 531; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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, MOLECULE TYPE:
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Sequence 3. Application US/09194905
Patent No. 6306627
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS
TITLE OF INVENTION: PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS
TITLE OF INVENTION: GLAO AND THEIR USE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                         7537 GCCGACATGGACGCCCTCCGCGAGCTCGCGGACCGGCACGGCCTGCACATCGTCGAGGAC 7478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7360 GICGICACCGGGGACCCCGAACCGCCGAACGGCICCGGAIGCTCCGCAACTACGCTCG 7301
                                                                                              GIGCAGCCCAGGTCGATCAGCGCGGACGCGG-CGGCCTGGCCCCCCTCCAGGGAGAACAG 4751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATA:
FLING DATE: 29-JUL-1998
FILING DATE: 29-JUL-1998
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APPLICATION NUMBER: WO PCT/EP97/02826
FILING DATE: 30-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19622783.6
FILING DATE: 07-JUN-1996
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 026083/0193
TELECOMMUNICATION INFORMATION:
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LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
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ZIP: 20007-5109
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7300 CGGCA 7296
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APPLICANT: Stockmann, Michael
APPLICANT: Taleghani, Rampiz Mansouri
APPLICANT: Distler, Jurgen
APPLICANT: Grabley, Susanne
APPLICANT: Sichel, Petra
APPLICANT: Brau, Barbara
TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them,
TITLE OF INVENTION: Use.
                                                                                          1149 GACGCCGTCCAGTGGTTGGTCACCTCCGGCGCGGACGTGCGCGCCACTACGACGGC
                                                                                                                                                                                                                                         GCGGGTGCCGTCGTCAGCAACTCCAGTGTCGGCCCGTACACCTCCATCGGGGAGGACTGC
                                                                                                                                                                                                                                                                                                                                                                                         2089 GCCATCCACCAGGCGGTGGCGGCCATCTCGCCCAGCAGCCGCGGCGAACTGGAGATCACC
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GCCGTCCACGAGGCGGTACGGGCCATCACCCCCTCCGCCGCGGCGGGGGTGGAGATCACC
                                                                     CACGCCGTGCAGTGGATGATCGACCGGGGCCTGCGCGTACGGGCCCGAGACCACCACCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.25
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PRIOR APPLICATION NUMBER: US 08/196,218
FILING DATE: 25-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OFFINE: PATCHLL....
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,953
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOFBRTING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5710032
GENERAL INFORMATION:
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STREET: 1300 I Street, N.W.
CITY: Washington
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CORRESPONDENCE ADDRESS
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8e-64;
~ 364;
           COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPILCATION NUMBER: US/08/196,218
FILING DATE: 25-AUG-1994
CLASSIFICATION: 435
                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OGGEN, Stasia L.
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 02481.1372-00000
TELECOMOUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPRAK: 202-408-4400
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66.3%; Pred. No. 8e-6
Live 0; Mismatches
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1561..2625
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416..1531
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3..401
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Best Local Similarity
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LOCATION:
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LOCATION:
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US-08-196-218-31
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2389 GCGGCCACGTCAGGACAGCCAGCTGGCCCCCACCACCGGCGGGGGGGACTGC 2448
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2916 CCCTGGCGCGACACCGGCAGCGCGGGAGGACATGCTGGAGGTCAACCGTCACGTCCTGGAC
                              2209 TACTGGAAGGACACCGGGAGGGTCGAGGACCTCTTGAGTGCAACACACCACCTCTGGAC
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                                                                                                      2976 GGACTGGAGGGCCGCATCGAGGGGAAGGTCGACGCGCCACACACCTGGTCGGCCGGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathry P.
APPLICANT: Crawford, Kathry P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
APPLICANT: Turner, Jan R.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dow AgroSciences LLC Patent Department STREET: 9330 Zionsville Road CITY: Indianapolis STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATES: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/09036987A Patent No. 6143526
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CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFENCE/DOCKET NUMBER: 50,1
TELECOMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 2310 base pairs
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EDNESS: double
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow Agros
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MEDIUM TYPE: Floppy
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Pred. No. 8e-64;
0; Mismatches 364; Indels
                                                 REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 02
                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS: LENGTH: 2634 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 66.3%;
Matches 716; Conservative
     ATTORNEY/AGENT INFORMATION:
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416..1531
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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US-08-681-953-31
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Pred. No. 2.9e-59;
0; Mismatches 297;
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                            tch 6.8%;
al Similarity 68.5%;
660; Conservative
                                                                                                                                                                                  1165..1992
                                                                              NAME/KEY: CDS
LOCATION: 88..1077
FEATURE:
                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-09-036-987A-25
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APPLICANT: Baltz, Richard H
APPLICANT: Baltz, Richard H
BOUGHCO, MATY C
APPLICANT: Broughton, MATY C
APPLICANT: Treadway, Pattl J
APPLICANT: Treadway, Pattl J
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-08-09
BARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0 9 Length 2310; Indels .8; DB 4; 2.9e-59; 0; Mismatches 297; Score 465.8; Pred. No. 2.9 TYPE: DNA ORGANISM: Saccharopolyspora spinosa Sequence 25, Application US/09370700 Patent No. 6274350 1 6.8%; Similarity 68.5%; Conservative ; NAME/KEY: CDS ; LOCATION: (1165)..(1992) US-09-370-700-25 LOCATION: (88)..(1077) 4298 GCC 4300 1054 GCC 1056 NAME/KEY: CDS Query Match Best Local Simi Matches 660; SEQ ID NO 25 LENGTH: 2310 SULT 8 -09-370-700-25 FEATURE: 4238 3458 3578 334 3638 394 3698 454 ó ð a 셤 ö 셤 ò 8 δ d ŏ g ò g ò 8 å

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APPLICANT: Betlach C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
TITLE REFERENCE: 30060-20030.00
CURRENT APPLICATION NUMBER: 05/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1998-11-05
SOFTWARE: PALENTION NOS: 12
SOFTWARE: PALENTIN OS: 12
                                                                                                                                            GACCCCCTGCTTCCGACCTCGCCGTACCCGGCCTCGAAGGCGGCCTCGGACCTCATGGCG
             CGCGCCTACCACCGCACCCACGGACTGCCGTGTGCATCACCCGCTGCTCCAACAACTAC
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Pred. No. 1.3e-57;
0; Mismatches 333;
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Patent No. 6303767
GENERAL INFORMATION:
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LENGTH: 1476
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                                                GCAGCCTCGCCCGCCTGCACGCGGTGCGTGACCATCCCGGCCTCACCTTCGTCCAGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US
Patent No. 6565202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
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2089 CCGCGCCAGTGACCGACCATATCAGCAAGCCCCGTAAATGGCTCGGCCGAACATCGGGCA 2030
                                                                                                                                               4239 CGCTGGCCGACACCGCGAAGTGGTACGAGCGGCACGAGGACTGGTGGCGTCCCCTGCTCG 4298
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                                                                                                                                                                                                                       908 GCTCGCGCGGGCCGTCCGCTGGTACCGGGAGAACCGCGGGCTGGTGGAGCCCCCTCAAGG 967
                          ACTINOPLANES Sp., PROCESS FOR THE ISOLATION THEREOF AND THE USE THEREOF
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Pred. No. 2.9e-48;
0; Mismatches 548; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACARBOSE BIOSYNTHESIS GENES FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Crueger, Anneliese; Piepersberg, APPLICANT: Wolfgang; Distler, Jurgen; and APPLICANT: Stratmann, Ansgar TITLE OF INVENTION: ACARBOSE BIOSYNTHESIS GITTLE OF INVENTION: THEREOF AND THE USE THE TITLE OF INVENTION: THEREOF AND THE USE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: SPRUNG HORN KRAMER & WOODS 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Actinoplanes sp. SE 50/110
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APPLICATION UNDBER: DE 195 07 214.6
FILING DATE: 02-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: Bayer FELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08606322
Patent No. 5753501
                                                                                                                                                                                                                                                                                                                     4299 CCGCGACATGACGTCGGGCCG 4319
                                                                                                                                                                                                                                                                                                                                                                                                           968 CGACCGCCCCCAGCTGCCCG 988
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Best Local Similarity 57.6%;
Matches 760; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WordPerfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (914) 332-184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Bravo 3/25s
OPERATING SYSTEM: DOS
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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STRANDEDNESS: Doub
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CITY: Tarrytown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGCCTCGCCCGCCTGCACGCGGTGCGTGACCATCCCGGCCTCCACCTTCGTCCAGGGCG 3518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 GCAACCGCGCAACCTCGCCCGGTGGACGCGGACCCGCGACTGCGCTTCGTCCACGGCG 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.5%; Score 447; DB 4; Length 1014; 66.8%; Pred. No. 1.5e-56; ative; 0; Mismatches 320; Indels
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
                                                                                     ER: US/09/105, 537A
                                                                                                                                                                      NUMBER OF SEQ ID NOS: 43.
SOFTWARE: FastSEQ for Windows Version 3.0.
SEQ ID NO 13.
LENGTH: 1014
                                                                                                                                                                                                                                                                                          7 TYPE: DNA CREATION CONTROL OF C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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STRANDEDNESS:
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US-09-194-905-4/c
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                                                                                                                                                   1849 GAAGCGTCGGCGGACCCTCGTTCGTTCGGGGGGGCGACATCTGTGACGAAGGTCTA 1790
                                                                                                                                                                                                                                                                                                                                 3599 GACCGCTCCATCACCGACAGCGGTGCCTTCACCCGCACCAACGTGCTGGGCACCCAGGTC 3658
                                                                                                                                                                                                                                                                                                                                                   CIGCICGACGCCGCCCCCCCCACGGIGTGCGCACCTICGIGCACGICICCACCGACGAG 3718
                                                                                                                                                                                               GCGGTGCGTGACCATCCCGGCCTCATCGTCCAGGCGACGTGTGCGACACCGCGCTC 3538
                                                                                                                                                                                                                                                                  GTCGACACGCTGGCCGCGCGCGCACGACGACATCGTGCACTTCGCGGCCGAGTCGCACGTC 3598
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                                                                                                                              TITATCGGGTCCCATTTTGTAACTTCCCTGATCAGTGGCGACATTGCCACACCCACAACCC
                             CCCATTGGCGGCATTGCTACAATCCCGGCGATGAAAATCTTGGTCACCGGCGGAGCCGGC
                                                                 TTCATTCGCTCCG------CCTACGTCCGCCGGCTCCTGTCGCCCGGGGCCCCCGGC
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                                                               4437 CACCAGTICCGGCAIGAAGACGAAIICGGIGCGCGGCGGCGGCGTICCGCICAICICCIC
                                                                                                           890 GAACGIGACACCCCGAICCCACCGGCAGIGGCAGCCGCIGCCACCCGTCCCGGIGCCG
949 GGCGAGCCGGTGCATCAGCGCGGCG-GCTGCAGCTCGGCGCGCGCTCACGTGAC
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Pred. No. 4.7e-32;
0; Mismatches 163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP97/02826
FILING DATE: 30-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19622783.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/194,905
FILING DATE: 29-JUL-1998
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                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09194905
Patent No. 6306627
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: ISOLATION OF TITLE OF INVENTION: PSEUDO-OLIGOSP
TITLE OF INVENTION: GLAO AND THEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Granados, Patricia D. REGISTRATION NUMBER: 33,683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: 11near
; MOLECULE TYPE: DNA (genomic)
US-09-194-905-4
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llarity 69.6%;
Conservative
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ATTORNEY/AGENT INFORMATION:
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NFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: PatentIr
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Best Local Similarity
Matches 374; Conserv
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3867785 ccgr-----acgrgadcarccagacgargcggrraccgracrcacgcccrgaccracg 3867838
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3542 GACACGCTGGCCGCGCGCGCACGACATCGTGCACTTCGCGGCCGAGTCGCACGTCGAC 3601
                                                                                                                                                        CGCTCCATCACCGACAGCGGTGCCTTCACCCGCACCAACGTGCTGGGCACCCAGGTCCTG 3661
                                                                                                                                                                                                                                            CTCGACGCCGCGCTCCGCCACGGTGTGCGCACCTTCGTGCACGTCTCCACCGACGAGGTG 3721
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                                                                                                                                                                                   357 GACCGGGTCATGGCCGGCCAGGACCAGGTCGTGCACCTCGCCGCCGAGTCGCACGTGGAC 298
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGACGTCCGGGTGACCCGCTGTTCGAACAACTTCGGCCCCCCACCAGCATCCCGAG 3898
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"n" bases at various positions throughout the
represent a, t, c or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 CTGGACGTGCGCATCACCCGCTGCTCCAACAACTACGGCCCCTACCAGCACCCGGGG
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
UNDBER OF SEQ ID NOS: 2
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OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
US-09-103-840A-2
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SOFTWARE: Patentin Ver. 2.1
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3868490 GACTGATGGACCGCGATCCGGACGACTTCGACCACGACCGCGTCGGCCACGACC 3868549
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                                                    Db 3867953 ATTTTGCCGCCGAATCCCATGTCGACAATGCACTGGACAATCCGGAGCCGTTTCTGCACA 3868012
                                                                                                                                                                    3868013 CCAACGTCATCGGGACCTTCACCATCCTGGAAGCGGTGCGACGCCACGGTGTGCG---CC 3868069
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                                                                                                            3636 CCAACGTGCTGGGCACCCAGGTCCTGCTCGACGCCGCGCTCCGCCACGGTGTGCGCACT 3695
                                                                                                                                                                                                                           3696 TCGTGCACGTCTCCACCGACGAGGTGTACGGCTCCCCTCCCGCACGGGGCCCGCCGCGGAGA 3755
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3576 ACTICGCGGCCGAGTCGCACGTCGACCGCCCCATCACCGGACAGCGGTGCCTTCACCCGCA
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APPLICANT: ARMENTROUT, RICHARD W.
TITLE OF INVENTION: DNA SEGMENTS ANI
TITLE OF INVENTION: POLYSACCHARIDE
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Patent No. 5854034
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261 MADISON AVENUE
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US-08-592-874-1
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3891 ATCCCGAGAAGCTCATACCGCGCTTCCTGACCAGCCTCCTGTCCGGCGGCGCACCGTTCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Sphingomonas sp. S88
US-09-096-942-2
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APPLICANT: Mikolajczak, Marcia
APPLICANT: Yamazaki, Motohide
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Best Local Similarity 56.4%;
Matches 589; Conservative
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                                                                                                                                                                                       SPETWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/592,874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 234.8; DB 2;
Pred. No. 4.1e-26;
0; Mismatches 377;
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/377,440 FILING DATE: 24-0AN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 34,400 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.4%;
Best Local Similarity 56.4%;
Matches 589; Conservative
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                             FILING DATE
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                                                                                                                                                            TCTACGGCAAGGGCGAGAATATCCGCGACTGGCTGTACGTCGACGATCACGCCGAAGGCGC
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25269 TCCCCGAGAAGCTGATCCCGCTGACCATCCTCAACGCGCTGGAAGGCAAGCCCCTGCCCG
                                                                                  TCTACGGCGACGGCGCCACGTGCGCGACTGGCTGCACGTCGACGACCACGTCAGGGCCG
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APPLICANT: Armentrout, Richard W
TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas
TITLE OF INVENTION: Carrying Genes from Xanthomonas Campestris
FILE REFERENCE: seq list for appl filed from pro. appl
CURRENT APPLICATION NUMBER: US/09/096,942
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Pred. No. 4.1e-26;
0; Mismatches 377; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        CGCTGCCCAACCTGGAGCTCACGCACCGGTTGCTCGCACTG-----
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Patent No. 6027925
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qq	b 24849		24908	
ď	у 3564		3623	
đ	b 24909	ACGTGGTGATGCACCTCGCCGCCGGGGGCGTCGATCGCTCGATCGA	24968	
VO.	у · 3624		3681	
đ	b 24969		25028	
οy	у 3682		3716	
đ	b 25029	- Ē-i	25088	
ογ	y 3717	AGGIGIACGGCICCCTCCCGCACGGGCCGCCGCGGAGAGCGACCCCCTGCTIC	3770	
<u>а</u>	b 25089	CGGCGACCTG	25148	
Οy	у 3771	CGACCTCGCCGTACGCGGCGTCGAAGCGGCCTCGGACTCATGGCGCTCGACCACCACCACCACCACCACCACCACCACCACCACCAC	3830	
đ	b 25149	CCTCCTCGCCCTATTCGGCGTCGAAGGCGGCCAGCGACCATCTGGTCCGCGCCTGGGGTC	25208	
ογ	у 3831	GCACCCACGCCTGGACGTCCGGTGACCCGCTGTTCGAACTTCGGCCCCCACCAGC	3890	
d	b 25209		25268	
Q.	у 3891	ATCCCGAGAAGCTCATACCGCGCTTCCTGACCAGCCTCCTGTCCGGCGGCACCGTTCCCC	3950	
a	b 25269	TCCCGAGAAGCTGATCCGCTGACCATCCTCAACGCGCTGGAAGGCAAGCCCCTGCCCG	25328	
ογ	у 3951		4010	
đ	b 25329	TCTACGGCAAGGCGAGAATATCCGCGACTGGTACGTCGACGTCACGCCAAGGCGC	25388	
٠ Oy	y 4011	TCGAACTCGTCCGCTGTCGGGCCGCCGGCGAGATCTACAACATCGGGGGCGCGCCTCTTTTTTTT	4070	
qa	b 25389	regegacearecaceacedecaegreeceacaegreerargreecegegegegegegegegegegegegegegegegeg	25448	
δý	y 4071	CGCTGCCCAACCTGGAGCTCACGGTTGCTCGCACTG	4111	
đ	b 25449	AGGGCACCAACTIGCAGGTCGTCGAGACGATCTGCGACCTGCTCGATCAGCGCATTCCGC	25508	
δŏ	y 4112	TGCGGCCCGGGCCCGGAGCGCATCGTCCACGTCGAGAACCGCAAGGGGCACG	4163	
qq	b 25509	TGAAGGATGGCAAGAAGCGCCGCGAGCTGATCACCTTCGTCACCGAT	25568	
δ	y 4164		4223	
d d	b 25569.	ACCGCCGCTACGCGATCGACGCGACCTAGGACTGGGAACTGGGAGGCCGAGG	25628	
δ	y 4224	CCGACTTCGCGACCGCGCTGGCCGACACCGCGAAGTGGTACGAGGGCCACGAGGACTGGT	4283	
q	b 25629	AGAATTTCGACACCGGCATC	25688	
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qq	b 25689	GGGGTCGATCCGCTCCGGCAAAT 25712		
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Search completed: May 29, 2003, 06:35:06

OLEN MANE BOYN SHILL

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SUMMARIES

7	 M	3	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Applit.	Sequence 13, Appl	Sequence 13, Appl	Sequence: 13, Appl	Sequence 13, Appl	Sequence 4, Appli	Sequence 373, App	Sequence 536, App	Sequence 11, Appl	Sequence 11, Appl	Sequence 11. Appl	Sequence 11, Appl	Sequence 4002, Ap	Sequence 1, Appli
US-09-922-683-7	US-09-988-384B-3	US-09-860-846-3	US-09-836-821-3	US-09-861-289-3	US-09-922-683-3	US-09-860-846-13	US-09-988-384B-13	US-09-836-821-13	US-09-861-289-13	US-09-922-683-4	US-09-738-626-373	US-09-738-626-536	US-09-860-846-11	US-09-988-384B-11	US-09-836-821-11	US-09-861-289-11	US-09-815-242-4002	US-09-939-964-1
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	RESULT 1 US-09-922-683-7 ; Sequence 7, Application US/09922683 ; Publication No. US20020192793A1	
•	GENERAL INFORMATION: APPLICANT: DECKER, Heinrich TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCEN	GLAUCESCENS
	CORRESPONDENCE ADDRES: CORRESPONDENCE ADDRESS: STREET: 3000 K street, N.W.	·
	STATE: D.C. COUNTRY: U.S.A. ZIP: 2007-5109 COMPUTER READBALE: FORM:	
	COMPUTER: EAPPY ULSA COMPUTER: IMP PC COMPATIBLE COPERATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION THRRER: ISS/09/922.683	
	FILING DATE: 07-Aug-2001 CLASSIFICATION: <unknown> PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/194,905 FILING DATE: 1999-12-01 APPLICATION NUMBER: DE 19622783 6</unknown>	
	FILING DATE: 07-JUN-1996 ATTORNEY/AGENT INFORMATION: NAME: Granados, Patricia D. REGISTRATION NUMBER: 33, 683 REFERENCE/DOCKET NUMBER: 026083/0193 TELECOMMUNICATION INFORMATION.	
	TELEPHONE: (202) 672-5300 TELEFAX: (202) 672-5399 INFORMATION FOR SQL ID NO: 7: SEQUENCE CHARACTERSTICS: TYPE: nucleic acid	•

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o d	4681	CACATGACGCGGTGCAGCCCAGGTCG 	4740
\text{3} \frac{4}{5}	4741	AGGAGAACAGCGAGTGCTGC	4800
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oy op	5041	GTGTCCGCGTGCAGTCCGGAGACGAAGAT 	5100
oy O	5101	TCCGTGAGTTCGTCCTCGGTCGAGCCGCCCGGGGTCTGCGTGGCGAGCACGGGCGTGTAG	5160 5160
oy op	5161	CCCTGACGCGTGAGCGCCTGCCCCATCACCTGGGCCAGTGCGGGAAGAAGAAGGGTTGTCC	5220 5220
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CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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Pred. No. 1.2e-98;
0; Mismatches 1181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09860846; Patent No. US20020164742Al
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
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Best Local Similarity 53.3%;
Matches 1475; Conservative (
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US-09-860-846-3
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ž q	2623 9628	GCCAATCGGCCGCCGATCCCGCGGCGGCCGGCTGCTGCTCACCCCGGTCGCGGACCCGT 2682	
<u>સ</u>	2683 9568	CCGCCTTCGGCGTCGCGGACGCGGGACGGGGACGTGCTGCGCTTGGAGGAGAAAC 2742	
à a	2743 9508	CCGACGTCCCGCGCAGCTCGCTCGTCGCGTGTACGCCTTCAGCCCGGCCGTCC 2802	
දු දි	2803	ACGAGGGGGTACGGGCCATCACCCCTCCGCGGGGGGGGGG	
à a	2863	TGCAGTGGATGATCGACCGGGGCCTGCGGGTGGGCCGAGACCACCGGCCCT 2919	
ž d	2920	GGCGCGACACCGGCAGCGCGGAGGACATGCTGGAGGTCAACCGTCACGTCTGGACGGAC	
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λa q	3040 9241	TGGCCGAAGGCGCGATCGTGGGGGTCACGTGGTGGGCCCGGTGGTGGTCGGCGGG 3099	
à a	3100	GTGCCGTCGTCAGCAACTCCAGTGTCGGCCGTACACCTCCATCGGGGAGACTGCCGGG 3159	
<u>ک</u> و	3160 9128	TCGAGGACAGCGCCATCGATACTCCGTCCTGCTGCGGGGGCCCAGGTCGAGGGGGGCGT 3219	
λα q	3220	CCCGCATCGAGGCGTCCCTCATCGGCCGGGGCGGTCGTCGGCCCGGCCCCCGTCTCC 3279	
ya da	3280		
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8618 8498 CATCGGGGGCGCACCTCGCTGCCCAACCTGGAGCTCACGCACCGGTTGCTCGCACTGTG 4113 4233 8018 4404 7957 GCCGAGACCCCCCCCCCCTCCTCGACCTCAAGGCCGCTACGAGGAGCTCCGCGCG 7898 CCCCGCGGCCGGCGCGGTGGACCCCCGGACCAC----CAGTTCCGGCATGAAGACGAA 4460 CCCCATCGCCTTGACGGCT-----GTCTGATGGTGGTCAGGGGACGTCGGTGAAG 4572 7777 AACAGCGGGATGGACGCCCTCCAGCTCGCCCTCGGGGCCTCGGCATCGGACCCGGGGAC 7718 CGCCGGCGCGCGCCCGCACGCCCCGAGGCCCATCATGTCGCTGCCGCACATGACGGCG 4692 7897 GAGACCGACGCGCGCATCGCCCGCGTCCTCGGGGCGCTACCTCCTCGGACCCGAA 7838 3574 GCACTTCGCGGCCGAGTCGCACGTCGACCGCTCCATCACCGACAGCGGTGCCTTCACCCG 3633 GCTCGCCGCGACATGACGTCGG------GCCGGACCGCAACCACCGGCCCCGGCCGG 4344 4174 CGCGGTCGACCACAGCAAGATCACCGCGGAACTCGGTTACCGGCCGCGCACCGACTTCGC GACCGCGCTGGCCGACACCGCGAAGTGGTACGAGCGCCACGAGGACTGGTGGCGTCCCCT 8017 caaggcgaccgcccgcagcrgccgccaccgccarcgcgrgaggrgrccgcgrgagcagc GAGGTGATCGTCCCTCGCACACGTACATCGCCAGCTGGCTCGCGGTGTCCCCCCACCGGC CACCAACGTGCTGGGCACCCAGGTCCTGCTCGACGCCGCGCTCCGCCACGGTGTGCGCAC 3754 GAGCGACCCCTGCTTCCGACCTCGCCGTACGCGGCGTCGAAGGCGGCCTCGGACCTCAT 3814 GGCGCTCGCCCACCGCACCGCACGCCTGGACGTCCGGGTGACCGCTGTTCGAACAA CGGCGCCACCGTTCCCCTCTACGGCGACGGGCGCACGTGCGCGACTGGCTGCACGTCGA CGGCGCGCGCGCGCGCGTCCGCGTCGAGAACCGCAAGGGGCACGACCGGCGCTA TTCGGTGCGCGGCGGCGTTCCGCTCATCTCCTCCAGCAGTGCGTCCACGGCGACCTG GCCATGAGCGGCGAGTCGTCGAAGCCGACCACCGAGATGTCACCGGGAACCGTGAGACCC 4054 8257 4234 4294 4405 4461 4573 7717 4114 8137 4521 4633 3694 3934 3634 qq à g g δ Q g à g 셤 g ŏ 셤 셤 ò a à g δ g ò Q ò g à ò õ g ò à ð g à ð g ò œ

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GIGGCCGCGTTCAGCTTCTACCCGGGCAAGAACCTCGGCTGCTTCGGCGACGCGGCGCCCC
                                   GTGCAGCCCAGGTCGATCAGCGCGGACGCGG-CGGCCTGGCCCCCCTCCAGGGAGAACAG
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APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Liu, Y.
APPLICANT: Liu, Y.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFRERENCE: 600, 4381051
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FRSESEQ for Windows Version 3.0
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Pred. No. 1.2e-98;
0; Mismatches 1181;
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; ORGANISM: Streptomyces venezuelae
US-09-836-821-3
                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/0983621 Publication No. US20030087405A1 GENERAL INFORMATION:
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Best Local Similarity 53.3%;
Matches 1475; Conservative
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                                                                                                                                                                                                                                                                                                       TGCAGTGGATGATCGACCGGGGCCTGCGCGTACGGGCCGA---GACCACCACCACGGCCCT
                                   2566 ACTICCTGCTGTACCTGGGGGACAACTACCTGCCC---CAGGGCGTCACCGACTTCGCCC
                                                                9688 ccrececcrearceresecacaacarcrecacesecesecesecreracaeserese
                                                                                                                                   9628 GGGACAGCATCGCGCGCCTCCACGCTGCGTGCTTCGGCTACCCGGTCAAGGACCCCG
                                                                                                                                                                       2683 CCGCCTTCGCCGTCGCGGAGGTCGACGCGGACGGGAACGTGCTGCGCTTGGAGGAAAC
                                                                                                                                                                                       CCGACGTCCCGCGCAGCTCGCTCGCGCTCATCGGCGTGTACGCCTTCAGCCCGGCCGTCC
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o o	3634	CACCAACGTGGTGGGCACCCAGGTCCTGGTCGGCGCTCCGCCACGGTGTGCGCAC 3693
Oy Dp	3694	CTTCGTGCACGTGCACCGACGAGGTGTACGGCTCCCTCCC
O. Db	3754 8557	GAGCGACCCCTGCTTCCGACCTCGCCGTCGGGCGCCTCGGACCTCGT 3813
Qy Dp	3814 8497	GGCGCTCGCCCACCGCACCCACGGCCTGGACGTCCGGGTGACCGCTGTTCGAACAA 3873
Oy Dp	3874	CTTCGGCCCCACCAGCATCCCGAGATCCGCGCTTCCTGACCAGCCTCCTGTC 3933
oy G	3934 8377	CGGCGGCACCGTTCCCCTCTACGGCGACGGGCACGTGCGCACTGGCTGG
9 9	3994	CGACCACGACGACGACGAGACTCGTCGGGTGTCGGGCGGG
g g	4054 8257	CATCGGGGCGCGCACCTCGCTGCCCAACTGGGGGCTCGCTGGCTG
e o	4114	CGGCGCGGGCCCGGAGCGCATCGTCGAGAACCGCAAGGGCACGGCGCTA 4173
Qy Dp	4 17 4 8137	CGCGGTCGACCACAGCAAGATCACCGCGGAACTCGGTTACCGGCCGCGCACCGACTTCGC 4233
Oy Dp	4234	GACCGCGCTGGCCGACGCGAAGTGGTACGAGCGGCACGAGGACTGGTGGCGTCCCCT 4293
Oy Dp	4294 8017	GCTCGCCGCGACATGACGTCGGGCCGGACCGCAACCACCGGCCCGGGCGGG 4344
oy Op	4345	CACACCGCCGCCGGGCGGTCGGCCGGTCAGCGTCGTGAGCCGGGGCGCGGCCG 4404
gy Gp	4405	CCCGCGGGCGGCGGCGGTGGACCCCCGGACCACAGTTCCGGCATGAAGACGAA 4460
Oy Dp	4461	TTGGGTGCGGGGGGGGTTCCGCTCATCTCCTCCAGGGGTGCGTCCACGGCGACCTG 4520
Oy Dp	4521	CCCCATCGCCTTGACGGGCTGTCTGATGGTGGTCGGGAGGGTCGGTGAAG 4572
합	4573	GCCATGAGCGGCGAGTCGTCGACCGACCGAGATGTCACCGGGAACCGTGAGACCC 4632
oy Oy	4633	CGCCGGCGCGCCGCCGCCGCCGAGGCCATCATGTCGCTGGCGCACATGACGGCG 4692

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13;
                                    7597 GAGAAGGGGATCACCCCCCCCCCGGGCGCTCCTCCCCGTCCTACGGGCACCCC 7538
                                                                                                               4872 GCCGACGCGTCGTGCCCCAGCTCCGCCAGGTGCGCCACGGCCAGGCGCATCGCGGCCCG 4931
                                                                                                                                                                                                                                                                                                   7420 GIGGCCGCGTICAGCTICTACCGGGCAACAACCICGGCTGCTICGGCGACGCGGCGCC 7361
                                                                                                                                                                                                                                                                                                                                                   4932 GICGICCGGGGAGACGAAGGGIGCCICGATCCGGGGCGAGAACCCGTICACGAGGACGAA 4991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9808 TCCAGTCGCTTCTCGGAAACGGCAGGCACCTGGGAATAGAACTCGACTATGCGGTCCAGA 9749
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4693 GTGCAGCCCAGGTCGATCAGCGCGGACGCG-CGGCCTGGCCCCCCTCCAGGGAGAACAG 4751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 1181; Indels 109; Gaps
                                                                                 4752 CGAGTGCTGCACGAGCTCCTCGGACTCCCGCGCGGACACTCCCCAGGTGCTCCCGCACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9928 TITCGAAGCAGATICTTCCGGTCTACAACAACCGATGATCTACTACTACTGCGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.7%; Score 527.4; DB 10; Length 13613; Best Local Similarity 53.3%; Pred. No. 1.2e-98; Matches 1475; Conservative 0; Mismatches 1181; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Xue, Y.
APPLICANT: Xue, Y.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600, 438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR PELLING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 13613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09861289
Patent No. US20020110897A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-861-289-3
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7300 CGGCA 7296
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8138 4460 4632 8618 3753 3813 3873 8438 8318 4053 8198 4173 4233 8078 4293 8018 4344 4404 7898 4520 GGCCGGCGCGCCCCGCACGCCCCAGGCCCATCATGTCGCTGCCCCACATGACGCCG 4692 CATCGGGGGGGGCGCCACCTGGCTGCCTGGAGCTCACGCACCGGTTGCTCGCACTGTG 4113 7837 CTCGAAGGATTCGAGGCGGAGTTCGCCGCGTACTGCGAGACGGACCACGCCGTCGGCGTG 7778 4521 CCCCATCGCCTTGACGGGCT-----GTCTGATGGTGGTCAGGGGAGGGTCGGTGAAG 4572 GAGGTGATCGTCCCCTCGCACACGTACATCGCCAGCTGGCTCGCGGTGTCCGCCACCGGC 7658 4693 GTGCAGCCCAGGTCGATCAGCGCGGACGCGG-CGGCCTGGCCCCCCTCCAGGGAGAACAG 4751 8017 CAAGGCGACCGCCCGCAGCTGCCCGCCACCGCGTGGAGGTGTCCGCGTGAGCAGCCGC 7958 TGCCCGGCCTACCACCGGACGTACGGCCTCGACGTACGGATCACCGCTGCTGCTGCAACAA CTTCGGCCCCGACCACCACCACGAGAGCTCATACCGCGCTTCCTGACCAGCCTCCTGTC GCCGAGACCCCCCGGGTCCCCTTCCTCGACCTCAAGGCCGCCTACGAGGAGCTCCGCGG 4405 CCCCGCGGGCGGCGGCGGTGGACCCCCGGACCAC----CAGTTCCGGCATGAAGACGAA 4461 TTCGGTGCGCGCGCGCGCGTTCCGCTCATCTCCTCCAGCAGTGCGTCCACGGCGACCTG GCGACCCCCGTGCCGCGCGCGCGAGGACCACCCCTGGACCCGCTGCTCGTC 8677 GACCAACGTGCAGGCCACGCAGACGCTGCTCCAGTGCGCCGTCGACGCCGGCGTCGGCCG GAGCGACCCCCTGCTTCCGACCTCGCCGTACGCGGCGTCGAAGGCGGCCTCGGACCTCAT GGCGCTCGCCCACCACCCCACGCCTGGACGTCCGGGTGACCCGCTGTTCGAACAA CGACCACGTCAGGGCCGTCGAACTCGTCCGCGTGTCGGGCCGGGCCGGGAGAGATCTACAA 4294 GCTCGCCGCGACATGACGTCGG------GCCGGACCGCAACCACCGGCCCGG GCCATGAGCGGCGAGTCGTCGAAGCCGACCACCGAGATGTCACCGGGAACCGTGAGACCC CITCGIGCACGICICCACCGACGAGGIGIACGGCICCCTCCCGCACGGGGCCGCGCGGA CGGCGCCCCCCTCTACGGCGACGGCGCACGTGCGCGACTGGCTGCACGTCGA CGGCGCGCGCGCGCGCGCGTCGTCCACGTCGAGAACCGCAAGGGGCACGACCGGCGCTA CGCGGTCGACCACACAAGATCACCGCGGAACTCGGTTACCGGCCGCGCACCGACTTCGC GACCGCGCTGGCCGACACCGCGAAGTGGTACGAGCGGCACGAGGACTGGTGGCGTCCCCT 7597 8377 8317 8077 4573 7717 4633 3694 8617 3754 8557 3814 8497 3874 8437 3934 3994 4054 8257 4114 8197 4174 4234 7957 7657 õ g g g ద ò 셤 g 셤 셤 셤 g g ò ŏ δ g ŏ δ à 셤 à 셤 ö g à à ð ŏ 셤 ð

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CCAGGTCCTGCTCGACGCCGCGCTCCGCCACGGTGTGCGCACCTTCGTGCAGGTCTCCAC 3711
                                                                           3412 CCCCGGCGCGTCGCGGTGACCGTCCTCGACAAACTCACCTACGCCGGCAGCCTCGCCCG 3471
                                                                                                                                                                                                                            CGCGCTCGTCGACACGCTGGCCGCCGCGCACGACGACGTCGTGCACTTCGCGGCCGAGTC 3591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGCACGCGGTGCGTGACCATCCCGGCCTCACCTTCGTCCAGGGCGACGTGTGCGACAC
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                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGTCCTGCTCGACGCCGCGCTCCGCCACGGTGTGCGCACCCTCGTGCACGTCTCCAC
 3352 CACCGGCGGAGCGGGCTTCATTCGCTCCGCCTACGTCCGCCGGCTCCTGTCGCCGGGC
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CURRENT APPLICATION NUMBER: 05/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR PLILING DATE: 1998-06-26
NUMBER OF SEO ID NOS: 43
SOFTWARE: PASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 447; DB 9; I
Pred. No. 3.4e-82;
0; Mismatches 320;
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Patent No. US20020164742A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
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66.8%;
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LENGTH: 1014
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                     4932 GTCGTCCGGGGAGACGAAGGGTGCCTCGATCCGGGGCGAGAACCCGTTCACGAGGACGAA 4991
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4752 GAGTGCTGCACGAGCTCCTCGGACTCCCGCGCCCGACACTCCCAGGTGCTCCCGCACGCC
                                                                       7477 GCCGCGAGGCCCACG---GCGCCCGCTACCGGGGCGGGCGGATCGGCGCGGGTCGTCG
                                                                                                                                              4872 GCCGACGCGCTCGTGCCCCAGGTCCGCCAGGCCCACGGCCAGGCGCATCGCGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09922683
Publication No. US20020192793A1
GENERAL INFORMATION:
APPLICANT: DECKER, Heinrich
TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,683
FILING DATE: 07-Aug-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 522.6; DB 9,
Pred. No. 1.6e-97;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/POCKET NUMBER: 026083/0193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLA.O AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION DATA:
APPLICATION NUMBER: 09/194,905
TLING DATE: 1999-12-01
APPLICATION NUMBER: DE 19622783.6
FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-922-683-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: '3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 97.4%;
Matches 531; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                               4992 GGGCA 4996
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Sequence 13, Application US/0998384B Publication No. US20030073824A1 GENERAL INFORMATION:

US-09-988-384B-13

RESULT 8

APPLICANT: Sherman, D.H. APPLICANT: Liu, H. APPLICANT: Xue, Y.

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 pikromycin
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Pred. No. 3.4e-82;
   and
TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.536US1
CURRENT APPLICATION NUBER: US/09/988,384B
CURRENT FILING DATE: 2001.11-19
PRIOR APPLICATION NUMBER: PCT/US99/14398
PRIOR FILING DATE: 1999-06-25
PRIOR PELION NUMBER: US 09/105,537
PRIOR FILING DATE: 1999-06-26
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 13
                                                                                                                                                          TYPE: DNA ORGANISM: Streptomyces venezuelae
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Best Local Similarity 66.8%;
Matches 655; Conservative
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APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Ane, Y.
TILLE APPLICANT: Ane, Y.
AITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/861,289
FILM DATE: 2001-05-18
PRIOR APPLICANTON NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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Pred. No. 3.4e-82;
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SOFTWARE: FastSEQ for Windows Version 3.0
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Matches 655; Conserv
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                                                            4179 TCGACCACAGCAAGATCACCGCGGAACTCGGTTACCGGCCGCGCACCGACTTCGCGACCG
                                                                                                    848 TCGACGCGCGCGAGATCGAGCGCGAGCTCGGCTACCGCCGCAGGTCTCCTTCGCGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA encoding methymycin and pik
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/836,821
CURRENT FILING DATE: 2001-04.17
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FRAESEQ for Windows Version 3.0
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Pred. No. 3.4e-82;
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09836821
Publication No. US20030087405A1
GENERAL INFORMATION:
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; ORGANISM: Streptomyces venezuelae
US-09-836-821-13
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           ACGIGIGCGACACCGCGCTCGTCGACACGCTGGCCGCGCGCGCACGACGACATCGTGCACT
                                                             ACATCCGCGACGCCGCCTCCTCGCCCGGGAACTGCGCGCGTGGACGCCATCGTCCACT
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 1.9e-47;
0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/POCKET NUMBER: 026083/0193
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: DE 19622783.6
FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/922,683
                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/194,905
FILING DATE: 1999-12-01
                                                                                                                                                                                                                                              FILING DATE: 07-Aug-2001
CLASSIFICATION: <Unknown>
                                                            COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     672-5399
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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nes 374; Conservative
STREET: 3000 K St
CITY: Washington
STATE: D.C.
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Similarity
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GENERAL INFORMATION
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SOFTWARE: Paten.
SEQ ID NO 536
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3842 CIGGACGICCGGGIGACCCGCIGITCGAACAACTICGGCCCCCACCAGCAICCCGAG 3898
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                 CTGGACGTGCGCATCACCCGCTGCTCCAACAACTACGGCCCCTACCAGCACCCGGGG 1
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Pred. No. 4.5e-33;
0; Mismatches 368;
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CURRENT FILING DATE: 2000-12-18
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FILING DATE: 1999-12-16
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-373
                                                                                                                                 Sequence 373, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                           MIZOGUCHI, HIROSHI
ANDO, SEIKO
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Best Local Similarity 56.1%;
Matches 497; Conservative
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TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI
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SOFTWARE: Patentin ver. 3.0
SEQ ID NO 373
LENGTH: 1131
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OCHIAI, KEIKO
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                                   649 AACAATTACGGTCCCTACCAGCACATTGAAAAGTTCATCCCCCGCCAGATCACCAATATT 708
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Pred. No. 1.3e-24;
0; Mismatches 579;
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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CURRENT FILING DATE: 2000-12-18
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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o. US20020197605A1
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ilarity 49.7%;
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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                                                                                                                     CICCGGGAAGGCACICAGCIGCGCG---AAIICAICGGGAAIGAIGGICTCGAIIICIIG 1033
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TGCAATGACCAGTGGTGGCAGCAGGCGGATGACGTTGCCATCGGTGCCGCAAGTCAGCAG 1210
                                                                                                                                                                     CTGGGGGAAGCGGGACTCCAGGGCGCGCAGCCGCTCCTGGATGAGCTCGCCGAGGACGCG 1016
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                                                                CAGCACACCTTCAGCTTTTGCGCGCGCGCACTGCGGCGGTTAAAGCTGCGTTCGGGCG
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Pred. No. 2.9e-23;
0; Mismatches 335; Indels
                                                                                                                                                                                                   pikromycin
                                                                                                                                                                                               TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.43804S1
CURRENA APPLICATION NUMBER: US/09/860,846
CURRENT FILLING DATE: 2001-05-18
                                                                                                                                                                                                                                    PRICR APPLICATION NUMBER: 2001-05-18
PRICR APPLICATION NUMBER: 09/105,537
PRICR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 879
                                                                              Sequence 11, Application US/09860846 Patent No. US20020164742A1 GENERAL INFORMATION: APPLICANT: Sherman, D.H.
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces venezuelae US-09-860-846-11
                                                                                                                                                                                                                                                                                                                                                                                                                               2.3%;
1larity 53.6%;
Conservative
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Matches 397; Conserva
144 GTCCACCACG 135
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Zhao, I
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US-09-860-846-11
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION: DNA encoding methymycin and pikromycin
ILE REFERENCE: 600.536US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/988,384B CURRENT FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US99/14398
                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/0998384B Publication No. US20030073824A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US (
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NUMBER OF SEQ ID NOS: 53
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US-09-988-384B-11
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                                                      482 ccercaaeccecerceaecreecercaecesecreraecreraecaecaecaece 541
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